

SHINE-DALGARNO MET

GGCCGCAAATTCATTTCAAGGAGACAGTCATAATG  
CGTTTAAGATAAAGTTCCTCTGTCAGTATTAC

LEADER SEQUENCE

AAATACCTATTGCCTACGGCAGCCGCT  
TTTATGGATAACGGATGCCGTCGGCGA

LEADER SEQUENCE

GGATTGTTATTACTCGCTGCCCAACCAG  
CCTAACATAATGAGCGACGGGTGTC

LINKER

LINKER

NCOI	V <sub>H</sub> BACKBONE	XHOI	SPEI
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CCATGGCCCAGGTGAACTGCTCGAGATTCTAGACTAGT  
GGTACCGGGTCCACTTTGACGAGCTCTAAAGATCTGATCA

TyrProTyrAspValProAspTyrAlaSer STOP LINKER  
TACCCGTACGACGTTCCGGACTACGGTTCTTAATAGAATTCG  
ATGGGCATGCTGCAAGGCCTGATGCCAAGAATTATCTTAAGCAGCT

FIG.1

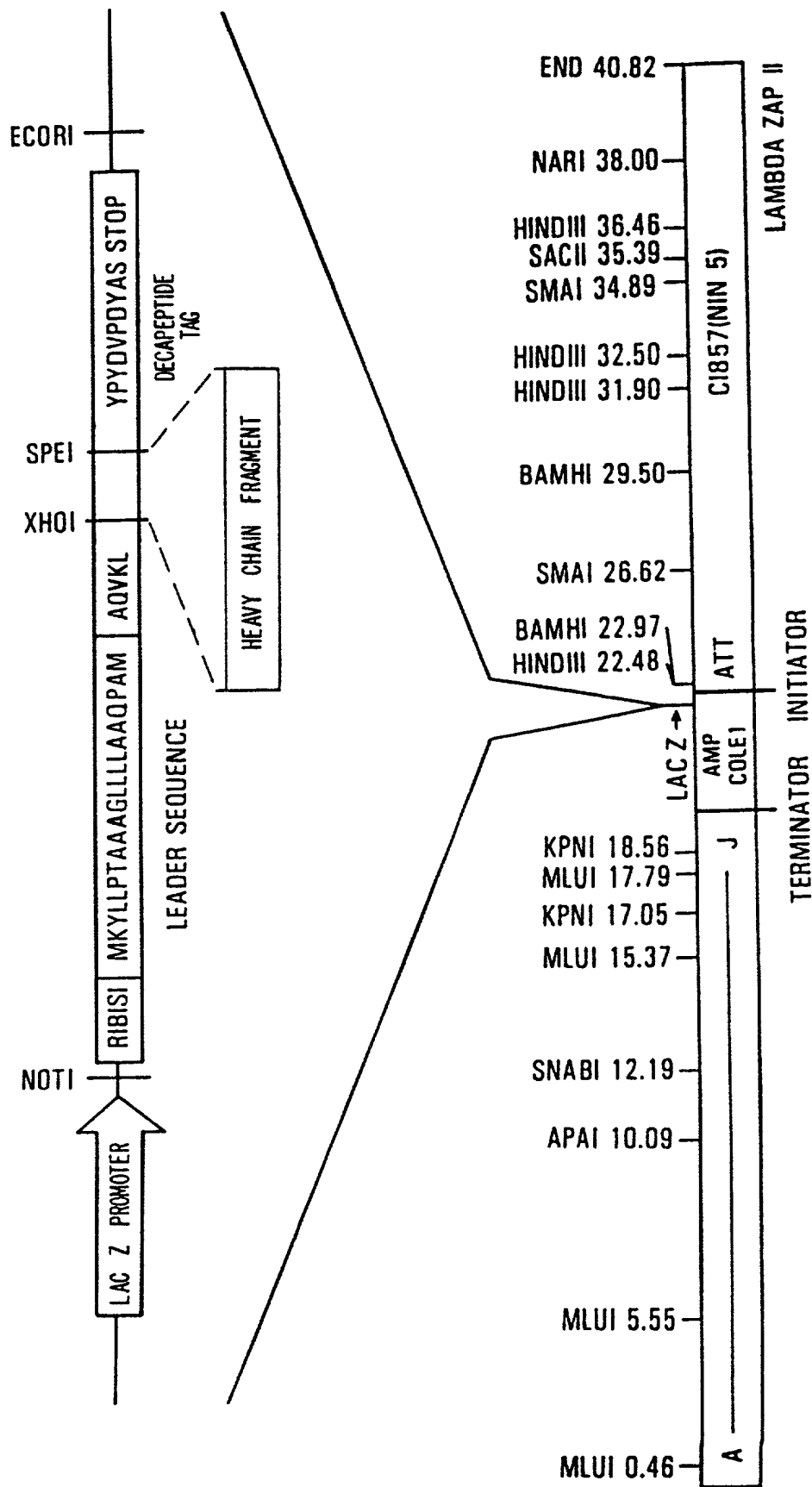


FIG.2

ECOR I SHINE-DALGARNO MET

## ECOR I

SHINE-DALGARNO MET

MET

TGAATTCTAACTAGTCGCCAAGGAGACAGTCATAATGAAATTCGAACTTAAGATTGTATCAGCGGTTCCCTCTGTCAGTATTACTTTA

## LEADER SEQUENCE

ACCTATTGCCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAG  
TGGATAACGGGATGCCGTCGGGACCTAACAAATAATGACGACGGTTGGTC

**NCO I**

**SAC I**

**XBA I**

Not I

CCATGGCCGAGCTCGTCAGTTCTAGAGTTAAGCGGCCG  
GGTACCGGCTCGAGCAGTCAAGATCTCAATTCCCGCGCAGCT

FIG. 3

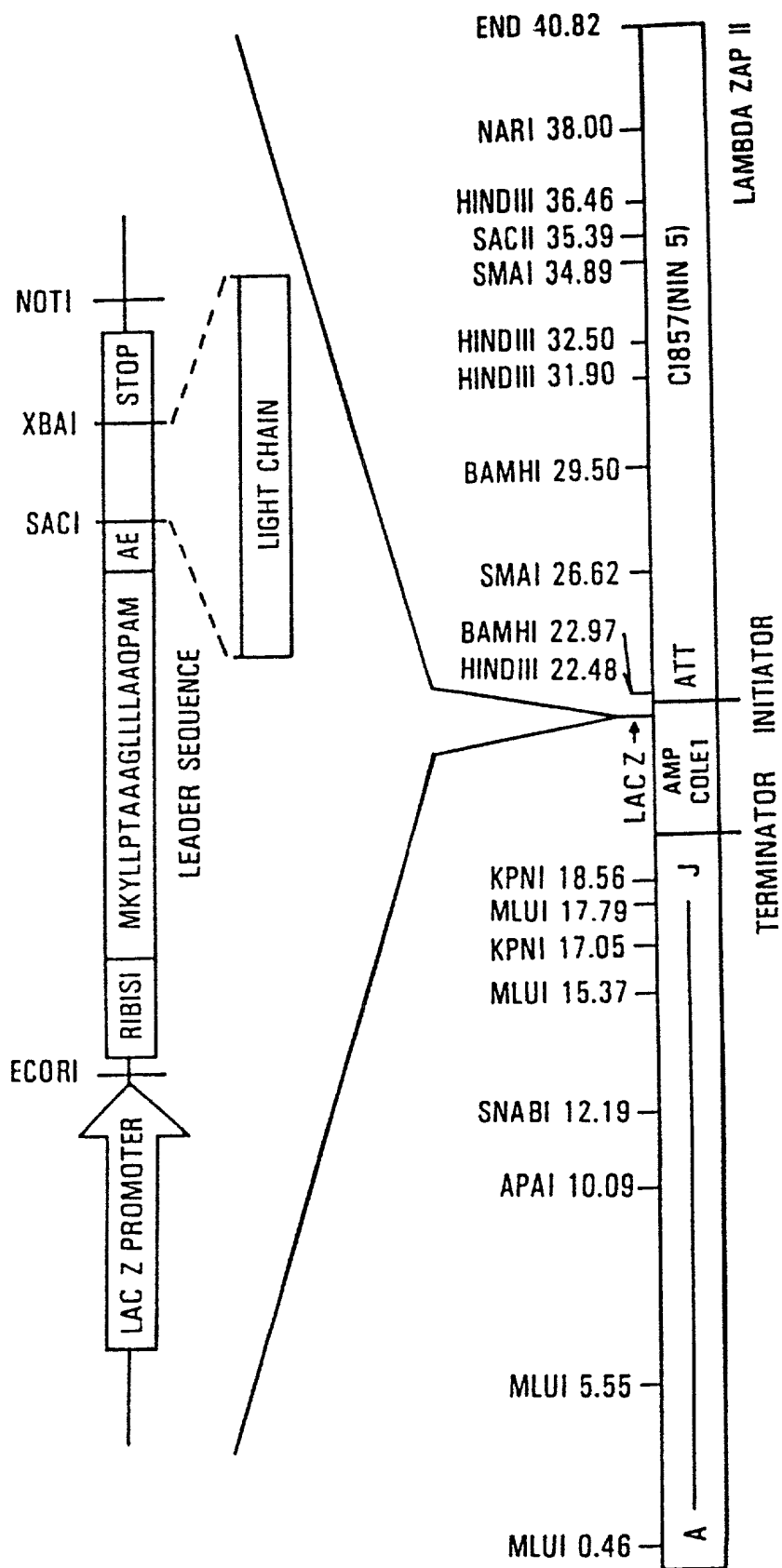


FIG. 4

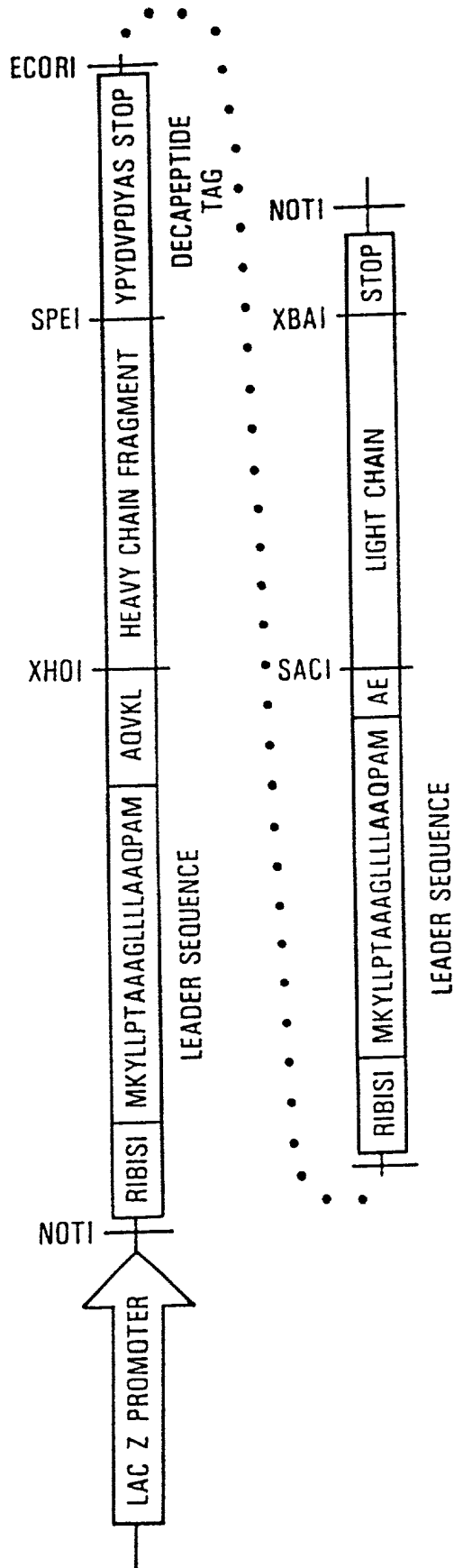
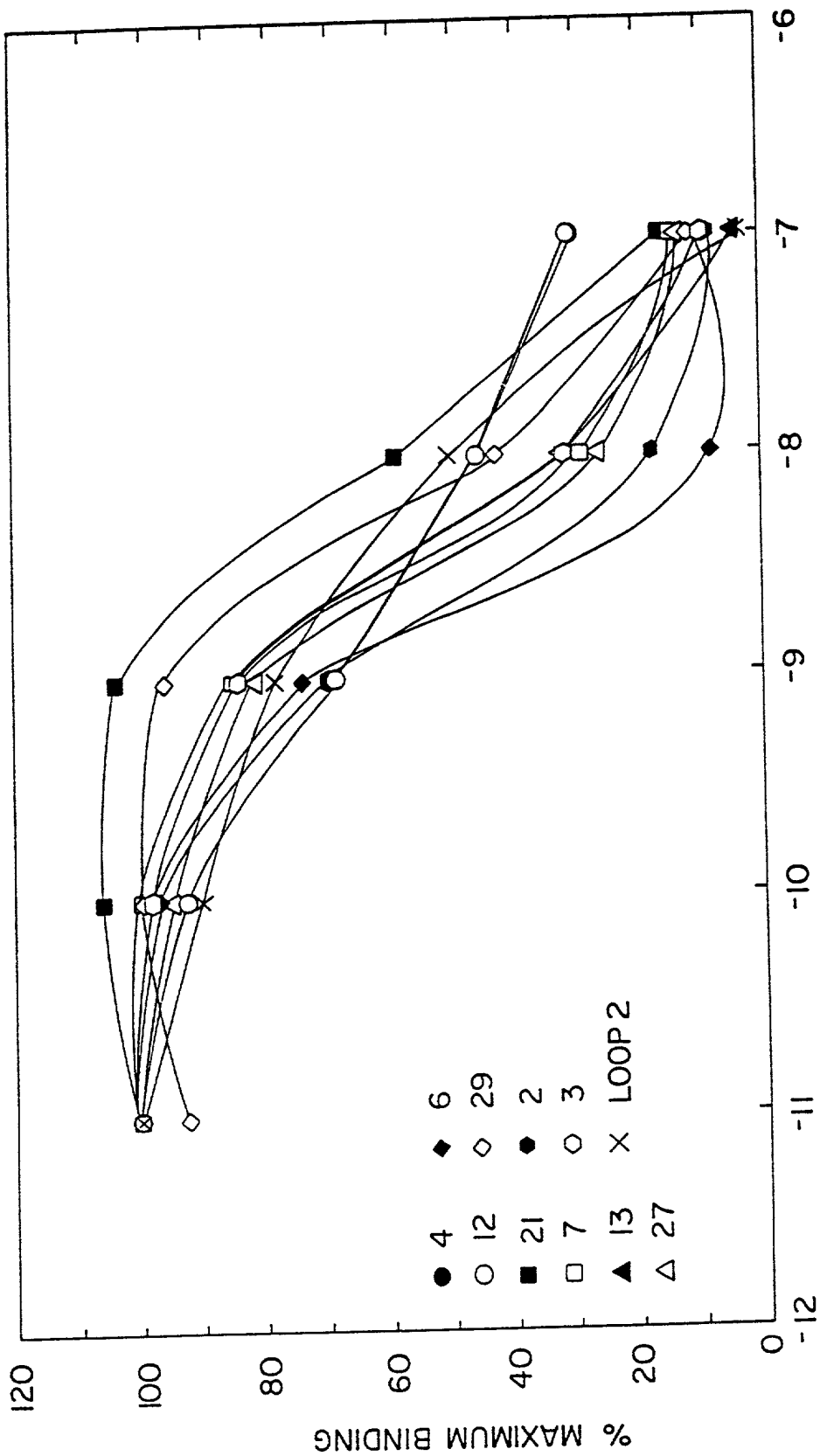


FIG.5

CLONE NO.	FAB CONCT ( $\mu$ g/ml)	ELISA TITER	<u>p24 ASSAY</u>		<u>SYNCYTIA ASSAY</u>
			<u>MN</u>	<u>IIIB</u>	<u>MN</u>
1	1.8	1:8	-	-	-
2	3.1	1:64	-	-	-
3	4.1	1:32	-	-	-
4	25.0	1:16	40	80	>128
5	2.4	1:128	-	-	-
6	4.0	1:64	-	-	-
7	4.5	1:64	20	20	32
8	14.0	1:256	20	20	-
11	11.0	1:128	-	-	-
12	6.0	1:64	80	40	>128
13	6.1	1:128	80	80	-
18	0.9	1:128	-	20	-
20	6.9	1:256	-	-	32
21	8.5	1:32	20	20	32
22	8.6	1:64	20	20	-
24	0.7	1:32	-	-	-
27	10.0	1:64	20	20	32
29	16.0	1:1024	-	-	-
31	9.3	1:128	-	-	-
35	8.9	1:64	-	-	-
2F5mAb	10.0		40	160	
2F5Fab	5.0		40	20	
F58mAb	10.0		160	40	
F58F(ab') <sub>2</sub>	200.0		40	20	

FIG. 6



LOG [COMPETING gp120]

FIG.7

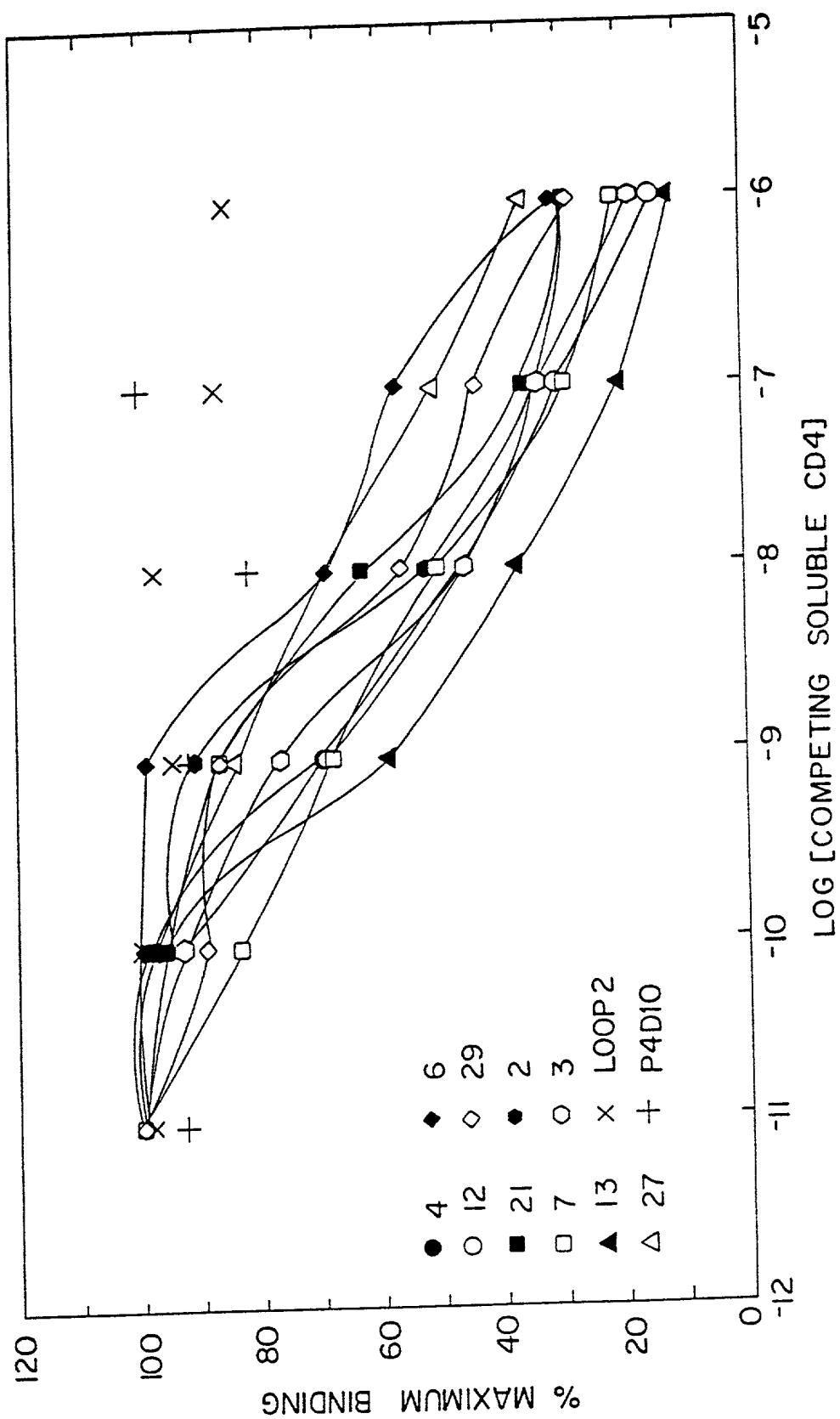


FIG. 8.

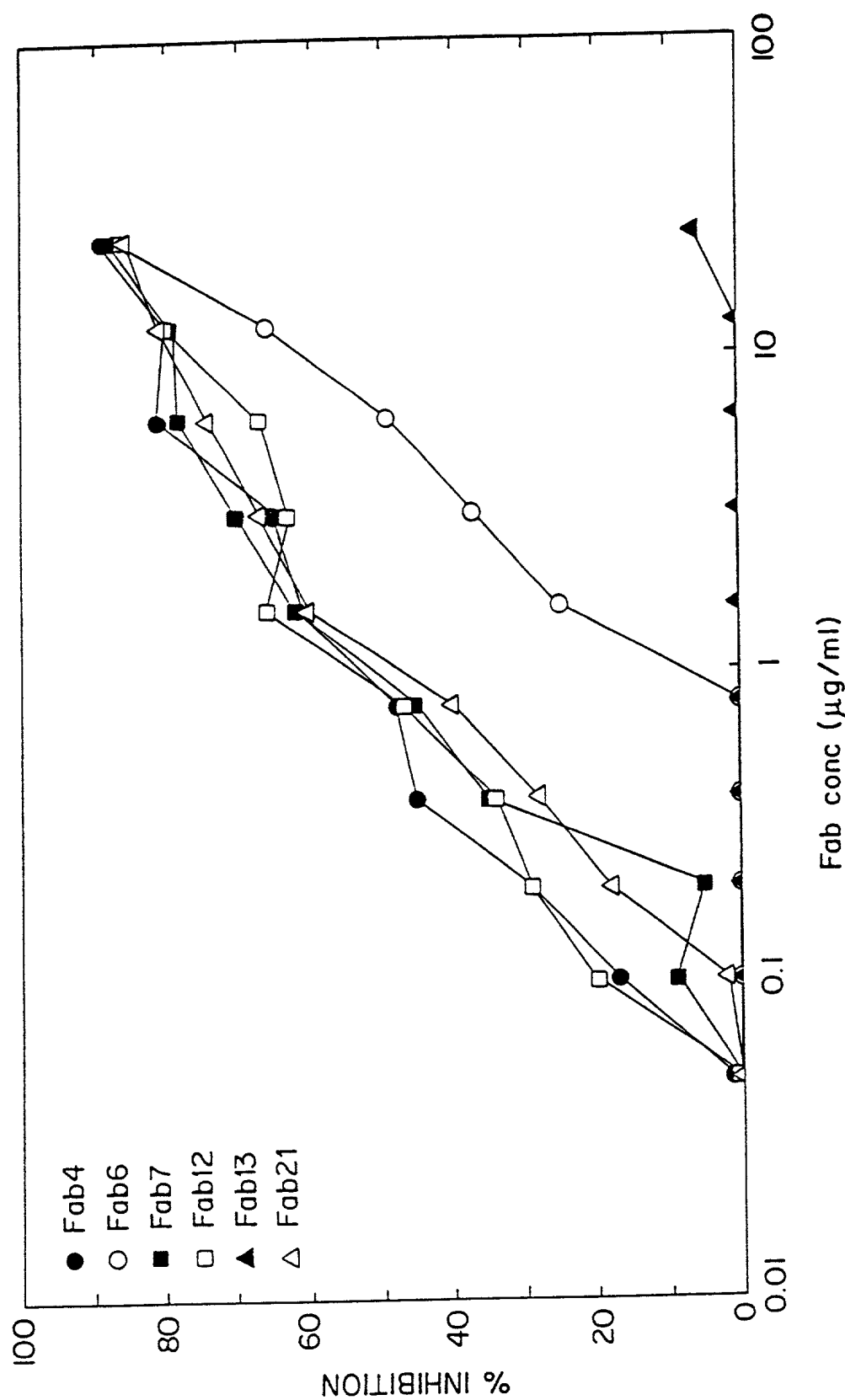


FIG. 9

Clone	FR1	CDR1	FR2	CDR2
b1	LEESGTEFKPPGSSVKVSKASGGTGG	DYASNYAIS	WVRQAPGGGLEIYG	GITPTSGSADYAQKFQG
b2	AAVQK	R...Q...D NF	WM	T.T.S
b14				
b24	A.V.K	I.S	M	T.T.S
B2	AAVQK	R...Q...D NF	WM	T.T.S
B30	Q.A.V.K	T...S	M	T
				A
b3	LEESGGRLVKPGGSLRLSCEGSGFTFT	NAWMT	WVRQSPGKGLEWVA	SIKSKFDGGSPHYAAPVEG
b5	Q			
B20	G			R
S2	A	S		
S3	S			
S5				S.PG
S7	G			
b4	LEQSGAEVKKPGASVKVSCQASGYRFS	NFVIH	WVRQAPGQRFEWMG	WINPYNGNKEFSAKFQD
b7				
b12				
b21				
b6	LEESGGGLVKPGGSLRLSCVSGSGFTFS	SAWMA	WVRQAPGRGLEWVG	LIKSKADGETTDYATPVKG
b20	A		G	
S6	I		K...I	
b8	LEESGEAVVQPGRSRLRLSCAASGFIFR	NYAMH	WVRQAPGKGLEWVA	LIKYDGRNKYYADSVKG
b13	Q	T		
b18	Q	T		
b22				
b27				
B26	Q	T		
B8				
B35	Q			
S4				
b11	LEQSGGGVVKPGGSLRLSCEGSGFTFP	NAWMT	WVRQSPGKGLEWVA	SIKSKFDGGSPHYAAPVEG
b29	E			
S8	LEESGGGLVQPGRSRLRVSCAASGFTFS	SYEMN	WVRQAPGKGLEWVS	QISSSGSRTYYADSVKG
100p35	LEQSGGGVVKPGRSRLRLSCAGSGFNFS	DDTMH	WVRQAPGKGLEWVA	VISYEGSDKYYADSVKG

FIG.10A

FR3	CDR3	J gene	SEQ ID NO
RVTISRDLRFTPIYMLRSLRIEDTAIYYCAR	ERRRGNPRALRGALDF	JH3	53
...APL...I...DD...V...	...V...V...		54
...AA...RV...S...V.F...	...EV...		55
...APL...I...DD...V...	...V...V...		56
...HE...V...SDQH...T...T...	...I...		57
			58
RFSISRNDLEDKMFLEMSGLKAEDTGVYYCAT	KYPRYSMDMTGVRNHFYMDV	JH6	59
...T...L...L...L...	...F...MA...L...		60
...T...L...L...L...	...MA...M...L...		61
...T...L...L...L...	...MA...M...L...		62
...T...YI...L...L...	...Y...MR...Y...		63
			64
			65
RVTFTADTSANTAYMELRSLRSADTAVYYCAR	VGYPYSDWDDSPQDNYYMDV	JH6	66
...D...D...D...D...	...T...T...T...		67
...D...D...D...D...	...T...T...T...		68
RFSISRNNLEDTVYLMQMSLRADDTAVYYCAT	QKPRYFDLLSGQYRRVAGAFDV	JH3	69
...T...N...N...N...	...S...YN...		70
...T...N...N...N...	...S...YN...		71
RFTISRDNKNTLYLQMNSLRAEDTAVYYCAR	DIGLKGHEYDILTAYGPDY	JH4	72
...S...S...S...S...	...E...E...E...E...		73
...S...S...S...S...	...E...E...E...E...		74
...S...S...S...S...	...A...A...A...A...		75
...S...S...S...S...	...A...A...A...A...		76
...S...S...S...S...	...A...A...A...A...		77
...S...S...S...S...	...A...A...A...A...		78
RFTISRNDLEDKVFLQMNGSLKAEDTGVYYCAT	RYPRYSEMMGGVRKHFYMDV	JH6	79
...S...S...S...S...	...S...S...S...S...		80
RFTISRDNKNSLYLEMTSLRVDDTAVYYCAR	GRRLVTFGGVVSGGNI	JH3	81
RFTISRDNSENTLYLQMSLSLRADDTALYYCAR	NTRENIEADGTAYYSYMDV	JH6	82

FIG. 10B

Clone	FR1	CDR1	FR2	CDR2
b1	ELTQSPSSLSASVGDRTITC	RASQGISNYLA	WYQKPGKVPRLLIY	AASTLQP
b2	.....I.....	.....N....	.....R.....	.....S
b14	.....I.....	.....N....	.....K.....	.....S
B2	.....GT.....	.....SVISNYLA	.....R...A.N....	.....S
b24	.....GT...L.P.E.A.LS.	.....SVISNYLA	.....QA.....	GV.NRAT
B30	.....GT...L.P.E.A.LS.	.....SVSNYYLA	.....R..QA.....	G..NRAT
b3	ELTQSPGTLSPGERATLSC	RASHRVNNFLA	WYQKPGQAPRLLIY	GASTRAT
b5	ELTQSPASVSASVGDITVTITC	RASQDIHNWLA	WYQKPGKAPKLLIY	AASSLQS
B20	ELTQSPGTLSPGERATLSC	RASQSLSNYYLA	WYQKPGQAPRLLIY	GSSTRGT
S2	QSPDTLSLNPGERATLSC	RASHRISSKRLA	WYQHKRGQAPRLLIY	VCPNRAG
S3	QSPSHLSLSPGERATLSC	RASQSVSAPYLA	WYQKPGQAPRLVIY	GASTRAT
S5	QSPGTLSPGDRATLSC	RASQSLSSSFLA	WYQKPGQAPRLLIY	SASMRAT
S7	QSPGTLSPGERATLSC	RASQSFSSNFLA	WYQKPGQAPRLLIY	VHPNRAT
b4	ELTQSPGTLSPGERATFSC	RSSHISIRSRVA	WYQHKPGQAPRLVIH	GVSNRAS
b7	.....T.....L...	.....L....	.....V.G.....L.Y	.....G
b12	.....A.....	.....N.....R	.....	.....
b21	.....A.....D.....	.....N.....	.....	.....
b6	ELTQSPGTLSPGERATLSC	RAGQSISSNYLA	WYQKPGQAPRLLIY	GASNRAT
S6	.....A.....A.....	.....S..L.N....	.....	.....S.T
b20	.....SS..A.V.D.V.IT.	.....TS.G..NYLA	.....KV.K....	.....TLQS
b8	ELTQSPSSLSASVGDRTITC	RASQSISSNYLN	WYQKPGKAPKLLIY	AASSLQR
b18	.....	.....N.N....	.....E.....H	T.FN..S
b22	.....	.....S....	.....	.....S
b27	.....	.....S....	.....	.....S
B35	.....	.....T.S....	.....	.....S
S4	.....	.....Q...D.R....	.....	.....D..NSET
b13	.....	.....Q...D..H..	.....	.....D..N.ET
B26	.....	.....T.N....	.....	.....G..N..S
B8	.....I.....	.....T.N....	.....	.....
b11	ELTQSPGTLSPGERATLSC	RASQSVNSNYLA	WYQKPGQTPRVVIY	STSRRAT
b29	.....	.....	.....	.....
S8	TQSPSSVSASVGDITVTFTC	RASQDIRNYLN	WYHQPKGKAPKLLIS	DASDLEI
loop35	SPGERATLSC	RASQSVGTNLA	WYQKPGQAPRLLIY	DASTRDT

FIG. 11A

FR3	CDR3	FR4	J gene	SEQ ID NO
GVPSRFGSGSGTDFLTISLQPEDVATYYC	QKYNAPRT	FGQGTKVEIKRT	JK1	82
...T...	...V...	...G...	JK4	83
...P...	...V.H...	...G...	JK1	84
...I.D...	...Q.GTS.W...	...G...	JK4	85
...I.D...	...Q.H.S.Y...	...L...	JK1	86
...A...	...	...	JK2	87
GIPDRFSGSGGTDFLTISRLEPDDFAVYYC	QQYGDSPLY	FGQGTKLEIKRT	JK2	88
GVPSRFGSGGTDFLTISLQPEDFAVYYC	QQGNSFPK	FGPGTVVDIKR	JK3	89
GIPDRFSGSGGTDFLTISRLEPEDFAVYYC	QHYGNSVYT	FGQGTKLEIKR	JK2	90
GVPDRFSGSGGTDFLTYSRLEPEDFAVYYC	QYGGSSYT	FGQGTKVEITR	JK2	91
DIPDRFSGSGGTDFLTISRLEPEDFAVYYC	QVYGGSPVL	FGQGTKLEMKR	JK2	92
GIPDRFSGSVGTDFLTISRLEPEDFAVYYC	QRFGTSPLYT	FGQGTKLEMKR	JK2	93
GVPDRFSGSGGTDFLTISRLEPEDFAVYYC	QQYGASLVS	FGPGTKVHIKR	JK3	94
GISDRFSGSGGTDFLTITRVEPEDFAVYYC	QVYGASSYT	FGQGTKLERKRT	JK2	95
...P...	...Q..S.R...	...I...	JK2	96
...	...	...	JK2	97
...	...	...DF...	JK2	98
GIPDRFSGSGGTDFLTISRLEPEDFAVYYC	QQYGTSPYT	FGQGTQLDIKRT	JK2	99
...G...	...N.V...	...K.E...	JK2	100
...S...	...N.DSA.W...	...KV...	JK1	101
GVPSRFGSGSGTDFLTISLQPEDFAVYYC	QQSYSIPPLT	FGGGTKVEIKRT	JK4	102
...TA...	...I.YT...	...Q...	JK2	103
...	...I.YT...	...L...	JK2	104
...	...I.QT...	...L...	JK2	105
...	...I.YT...	...L...	JK2	106
...G...	...T.YT...	...L...	JK2	107
...R...	...HQN.V.LT...	...	JK4	108
...FT...	...YDNL.LT...	...	JK4	109
...NT...	...NT..WT...	...Q...	JK1	110
...F...	...	...	JK2	111
GVPDRFSGSGGTDFLTISRLEPEDFAVYYC	QQFGDAQYT	FGQGTKLEIKRT	JK2	112
...	...	...	JK2	113
GVPSRFGSGSATYFSFTISLQPEDIGTYYC	QQYADLIT	FGGGTKVEIKRT	JK4	114
YIPDTFSGSGGTDFALTISLQSEDFGFYYC	QQYDNPPT	FGQGTKLEVKRT	JK2	115

FIG. 11B

Clone	FR1	CDR1	FR2	CDR2
HIV-H12/L12	ELTQAPGTLSPGERATFSC	RSSHISRVR	WYQHKPGQAPRLVIH	GVSNRAS
HIV-H12/LC11	....S.....D.....	....N.....A	.....	.....
HIV-H12/LC24	....S.....D.....	....N.....A	.....	.....T
HIV-H12/LC22	....S.....	....N.....A	.....	.....
HIV-H12/LC1	....S.D....NV.....L..	.A..R.S...LA	....R.....L.Y	...S..G
HIV-H12/LC7	....S.D....NA.....L..	.A..R.S...LA	....R.....L.Y	...K..G
HIV-H12/LC28	....S.D....NT.....L..	.A..R.G...LA	....RR.....L.Y	...K..G
HIV-H12/LC13	....S.....T.....IL..	KT..N.W...LA	...L.S.....L.Y	...K..G
HIV-H12/LC3	....S.....T.....IL..	KT..N.W...LA	...L.S.....L.Y	...K..G
HIV-H12/LC5	....S.....T.....IL..	KT..N.W...LA	...L.S.....L.Y	...K..G
HIV-H12/LC26	....S.....ST.....IL..	KT..N.W...LA	...V.S.LP...L..	...R..G
HIV-H12/LC25	....S.....N.....VL..	.T.RN.W...LA	...VRR.....L..	...K..G
HIV-H12/L12	ELTQAPGTLSPGERATFSC	RSSHISRVR	WYQHKPGQAPRLVIH	GVSNRAS

FIG.12A

FR3	CDR3	FR4	SEQ ID NO
GISDRFSGSGGTDFTLTITRVEPEDFALYYC	QVYGASSYT	FGQGTKLERKR	97
.....L.....	.....	.....DF..	114
.....L.....	.....	.....DF..	114
.....L.....	.....	.....DF..	115
VP.....S...S.L.....M...	T..G....	.....VDI..	116
VP.....S...S.L.....I...	T..G....	.....TVDI..	117
VP.....S...S.L.....I...	T..G....	.....VDI..	118
..P.....A.....S.....V...	T..G.A...	.....DI..	119
..P.....A.....S.....V...	T..G.A...	.....DI..	119
..P.....A.....S.....V...	T..G.A...	.....I...	120
..P.....AR.....S.L..A...V...	T..G....S	.....DFN.	121
..VP.....AR.....S.L.....V.F.	T..G....	....N..DIR.	122
GISDRFSGSGGTDFTLTITRVEPEDFALYYC	QVYGASSYT	FGQGTKLERKR	97

FIG.12B

	FR1	CDR1	FR2	CDR2
H12/L12	LEQSGAEVKKPGASVKVSCQASGYRFS	NFVIH	WVRQAPGQRFEWMG	WINPYNGNKEFSAKFQD
HC1	QVKL.....	...L.	.A.....H.P....	....A..VT.IPP....
HC2	QVKL.....	...L.	.A.....H.P....	....A..VT.I.P....
HC3	QVKL.....	...L.	.A.....H.P....	....A..VT.I.P....
HC7	QVKL.....I.....T	...L.	.A.....P....	.F..A..I..I.P....
HC9	QVKL.....	...L.	.A.....H.P....	....A..VT.I.P....
HC10	QVKL.....L.....	...L.	.A.....H.P....	....A..VT.I.P....
HC11	QVKL.....T.....I..K.....T	..PL.	.....P....	..KIV..E.KY.Q...V.
HC12	QVKL.....	....	.....	.....R.
HC13	QVKL.....	...L.	.A....T.DL....	....A..V..I.P....
HC14	QVKL.....	...L.	.A.....H.P....	....A..VT.IPP....
H12-L12	LEQSGAEVKKPGASVKVSCQASGYRFS	NFVIH	WVRQAPGQRFEWMG	WINPYNGNKEFSAKFQD

FIG.13A

FR3	CDR3	FR4	SEQ ID NO
RVTFTADTSANTAYMELRSLRSADTAVYYCAR	VGPSWDDSPQDNYYMDV	WGKGTTIVSS	66
..SL.R...G.V.L..TN..F.....	..EWT.....	.....T.	123
..SL.G...S.V.L..N..F.....	..EWT.....	..R....T	124
..SL.G...S.V.L.....F.....	..EWT.....	.....	125
..S..G...S...V...N.....	..PWT.....	.....	126
..SL.G...S.V.L..N..F.....	..EWT...F.....	.....	127
..SL.G...S.V.L..N..F.....	..EWT.....	.....T	128
....T.....V.G.....T.....	..EWT..MD..A.....	.....T	129
.....D.....I.....	....T.....	.....	130
..SL.G...S.V.L.....F.....	..EWT.....	.....	131
..SL.R...G.V.L..TN..F.....	..EWT.....	.....	132
RVTFTADTSANTAYMELRSLRSADTAVYYCAR	VGPSWDDSPQDNYYMDV	WGKGTTIVSS	66

FIG. 13B

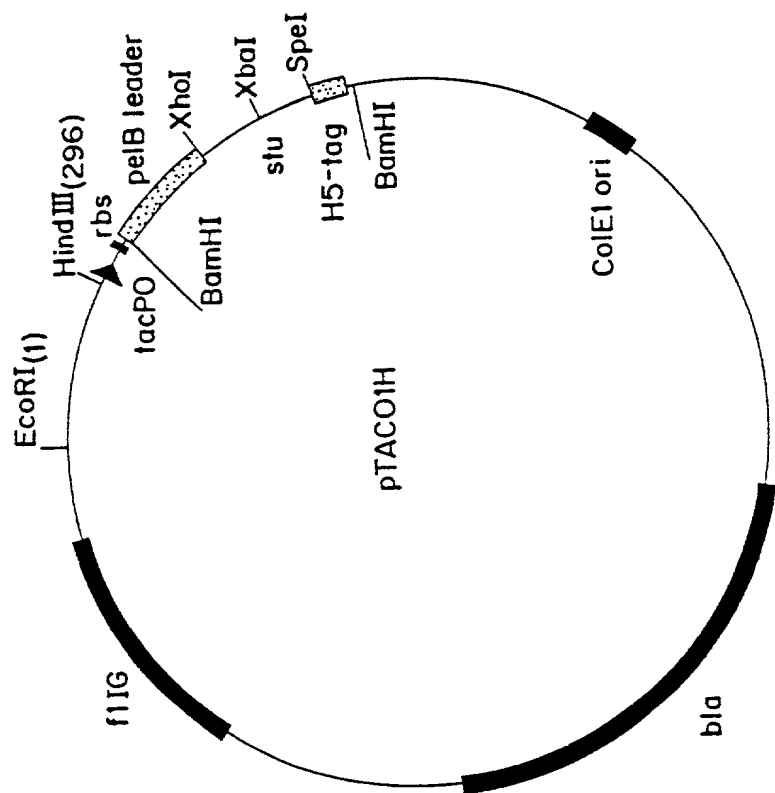


FIG. 14A

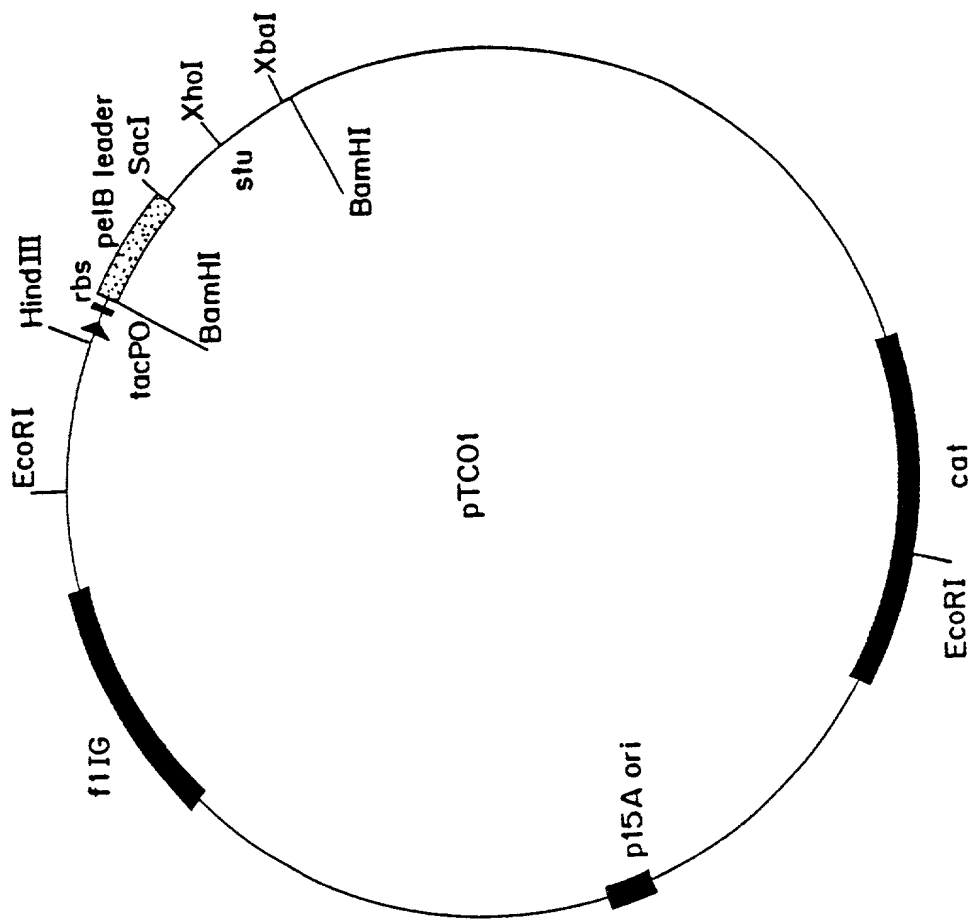


FIG. 14B

tac promoter  
 rbs BamHI pelB leader  
 MetLysTyrLeuLeuProThrAlaAlaAlaGly  
 TGTGACAAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACACAGGAGGAAGGATCCATGAAATACCTATTGCCTACGGCAGCCGCTGGA  
 ACACTGTTAATTAGTAGCCGAGCATATTACACACCTTAACACTCGCCTATTGTTAAAGTGTGTCCTCCCTCCTAGGTACTTTATGGATAACGGATGCCGTGCGGACCT  
 LeuLeuLeuLeuAlaAlaGlnProAlaMetAlaGluLeu  
 SacI XhoI XbaI  
 STOP  
 LeuLeuLeuLeuAlaAlaGlnProAlaMetAlaGluLeu  
 TTGTTATTACTCGCTGCCCAACCAAGCCATG6CCGAGCTCGGTGCGTCCCTCGAGGGTCGGTCGGTCCTCCTAGAGTTAAGCGGCCG  
 AACATAATGAGCGACGGGTTGGTCGGTACCGGCTCGAGCCAGCCAGGAGCTCCAGCCAGCCAGAGATCTCAATTCGCCCGGCG

FIG.15A

tac promoter  
 rbs BamHI pelB leader  
 MetLysTyrLeuLeuProThrAlaAlaAlaGly  
 TGTGACAAATTAATCATCGGCTCGTATAATGTGTGGAATTGTGAGCGGATAACAATTTACACACAGGAGGAAGGATCCATGAAATACCTATTGCCTACGGCAGCCGCTGGA  
 ACACTGTTAATTAGTAGCCGAGCATATTACACACCTTAACACTCGCCTATTGTTAAAGTGTGTCCTCCCTCCTAGGTACTTTATGGATAACGGATGCCGTGCGGACCT  
 LeuLeuLeuLeuAlaAlaGlnProAlaMetAlaGlnValLysLeuLeuGlu  
 XhoI SpeI (His)<sub>5</sub>-tail  
 ThrSerHisHisHisHisHisSTOP  
 LeuLeuLeuLeuAlaAlaGlnProAlaMetAlaGlnValLysLeuLeuGlu  
 TTGTTATTACTCGCTGCCCAACCAAGCCATG6CCCAAGGTGAAACTGCTCGAGGGTCGGTCGGTCCTCCTAGAGTTAAGCGGCCGCTGGA  
 AACATAATGAGCGACGGGTTGGTCGGTACCGGCTCGAGCCAGCCAGAGATCTGCCAGCCAGCCAGGATCAGTAGTAGTAGTAATTCGAT

FIG.15B

	b11	b6	* b4	* b12	* b7	b21	b3	q b13	q b22	q B26	S b8	S b18	S b27	S B8	S B35	S s4	Y b1	Y b14	Y b24	s8	p35
b11	+	+	w	+	+	-	+	+	-	-	-	-	-	-	-	-	+	-	-	-	-
b6	+	+	+	+	+	-	+	+	-	-	-	-	-	-	-	-	+	+	+	-	-
b4	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-
b12	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-
b7	+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	w	-	-	w	-
b21	+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	-	-	-	-
b3	+	+	-	+	+	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-
b13	w	w	-	+	+	-	-	+	+	+	+	+	+	+	+	+	-	-	-	w	-
*b22	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-
B26	w	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-
b8	+	+	+	+	+	-	w	+	+	+	+	+	+	+	+	+	-	-	-	-	-
b18	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	w	-	-
b27	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-
B8	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-
*B35	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-
s4	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	-	w	-	-
b1	+	+	+	+	+	-	-	+	w	-	+	w	-	-	-	-	+	+	+	-	-
b14	w	+	+	+	+	w	-	+	-	-	+	-	-	-	-	-	+	+	+	-	-
b24	+	+	+	+	+	-	+	-	-	-	+	-	-	-	-	-	+	+	+	-	-
s8	w	+	+	+	+	-	w	+	+	w	+	+	+	+	+	+	-	-	-	+	-
p35	+	+	+	+	+	-	+	w	w	w	+	w	w	w	w	+	w	-	-	-	+

FIG.16

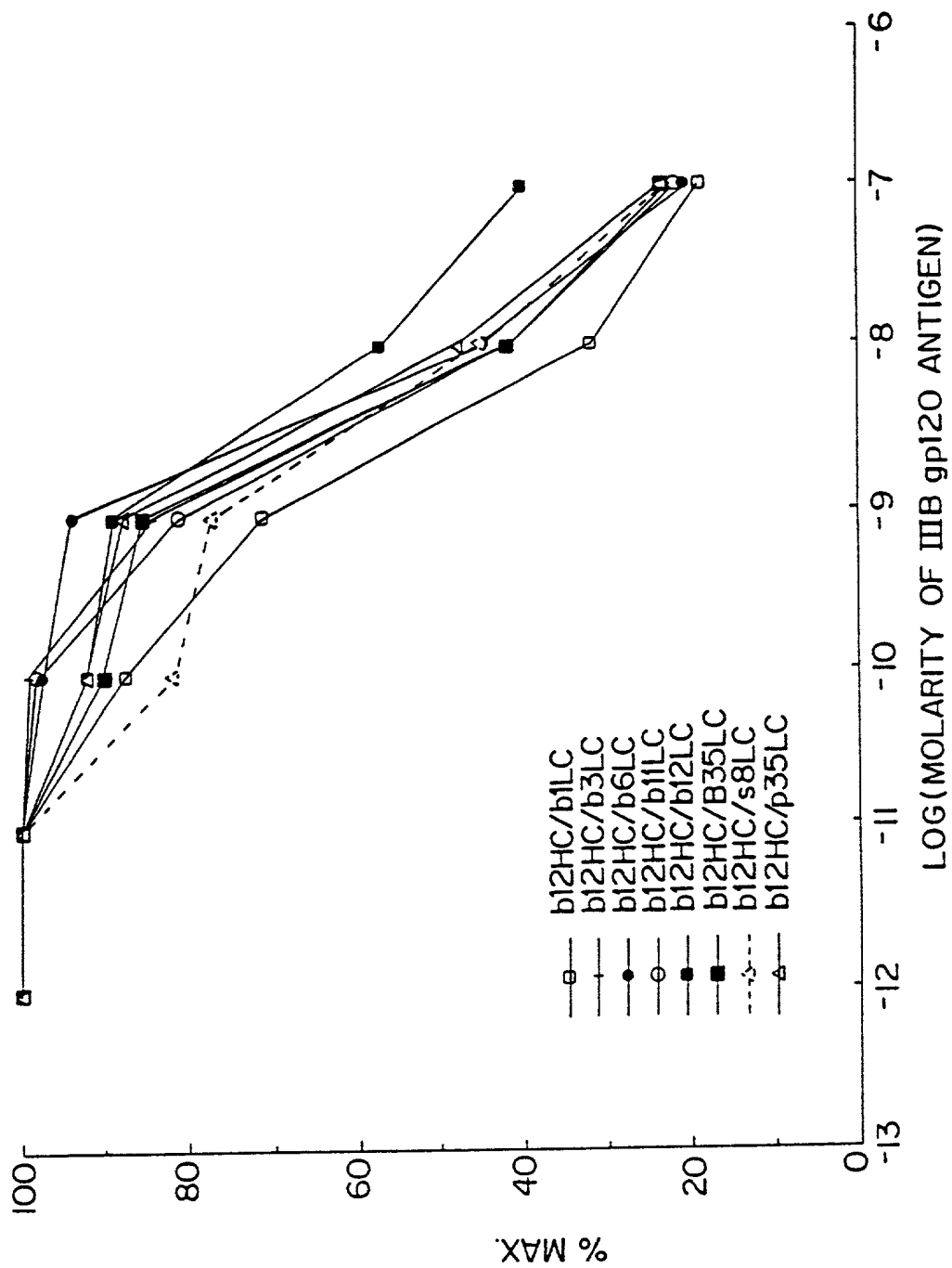


FIG.17

CLONE	FR1	CDR1	FR2	CDR2
DL 41 19	LLESGPGLVKPSETLSLTCTVSGGSL	SFDWN	WIRQAPGKGLEWIG	RIYPSGNTHYNPSLRS
DO 41 11	LLKSGGGLVKPGGSLRLSCVISAFSFS	GYNIN	WVRQAPGKGLEWVS	SISMSTGSLSYADSMKG
GL 41 1	LLESGGGLVKPGGSLRLSCSASGFTFS	SYGMN	WVRQAPGKGPEWVA	YISSSRKYTEYADSVKG
MT 41 12	LLESGGGLVQPGGSLRISCVASGDIIFYSYAMS	WVRQAPGKGLEWVA		SISGTGGSNYYADSVKG
SS 41 8	LLESGGGLVQPGGSLRLSCAASGFLYS	SFAMS	WVRQAPGKGLEWVS	TISASGGSTKYADSVKG

FIG. 18A

FR3	CDR3	FR4
RVTMSRDTSKNQFSVKLTSVTAADTALYYCAR	ENTGRTIEEIGNFFDI	WGQGLTVTVSSASTKG
RFTISRDNKNSVYLEMSSLTAEDTAMYYCAA	RTPLVGRALDI	WGQGLTVTVSSASTKG
RFTISRDNKNSVFLQLDSLTAEDTAIYYCAR	GRDFYSGFGRRDDFHLHYMDV	WGKGTTVTVSSASTKG
RFTISRDNKSTLYLQMNSLRAEDTALYYCAR	DRGPRIGIRGWFD	WGQGLTVTVSSASTKG
RFTISRDNKNTIYLQMDSLRAEDTAVYYCAK	NFRAFARDPWGD	WGQGLTVTVSSASASTK

FIG. 18B

CLONE	FR1	CDR1	FR2	CDR2
DL 41 19	MAELTQSPGTLSPGERVIVSC	RASQSVSSNYLA	WYQQKPGQAPRLLIY	GASNRAT
DO 41 11	MAELTQSPGTLSPGERATFSC	RSSHSHIITRRVA	WYQHKPGQAPRLVIH	GVSNRAS
GL 41 1	MAELTQSPGTLSPGERATLSC	RASQSVSNGYLA	WYQQKPGQAPRLLIY	GASTRAT
MT 41 12	MAELTQSPSSLSASVGDRVTITC	RPSQIGIRFFN	WYQQKPGKAPNLLIY	AADILQS
SS 41 8	MAELTQSPSSLSASVGDRVTITC	RASQGVSSSYLA	WYQQKPGQAPRLVIF	GAYS RAT

FIG. 19A

FR3	CDR3	FR4
GIPDRFSGSGGTDFTLTISRLEPEDFAVYYC	QQYGSSGT	FGQGTKVEIKRT
GISDRFSGSGGTDFTLTITRVEPEDFALYYC	QVYGASSYT	FGQGTKLERKRTVY
DIPDRFSGSGGADFTLAI SRLEPEDFAVYYC	QQYAGSHT	FGQGTKLEIKRTVA
GVPSRFSGSGGTDFTLTISLQPEDFATYYC	QQSYSTPYT	FGQGTRLDIKRTVA
GIPDRFSGSGGTDFTLTISRLEPEDFAVYYC	QQYGSSPIT	FGPGTKVDIKRTVA

FIG. 19B

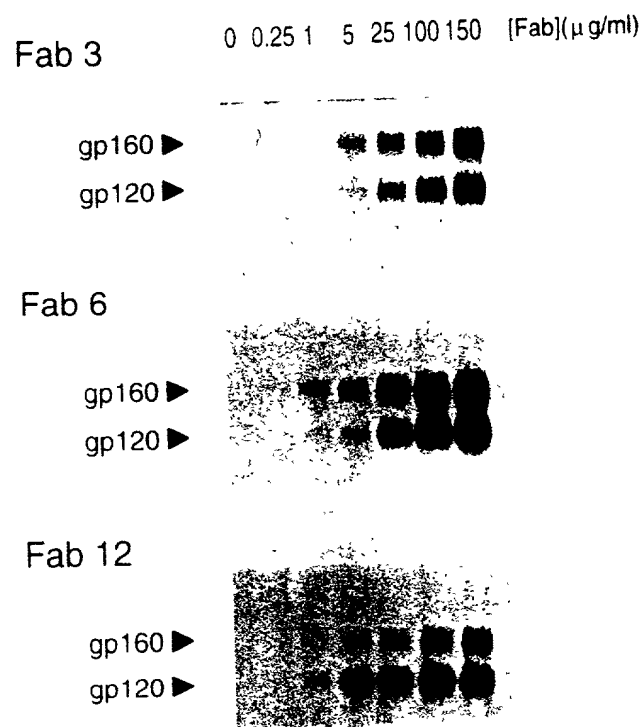


FIG. 20

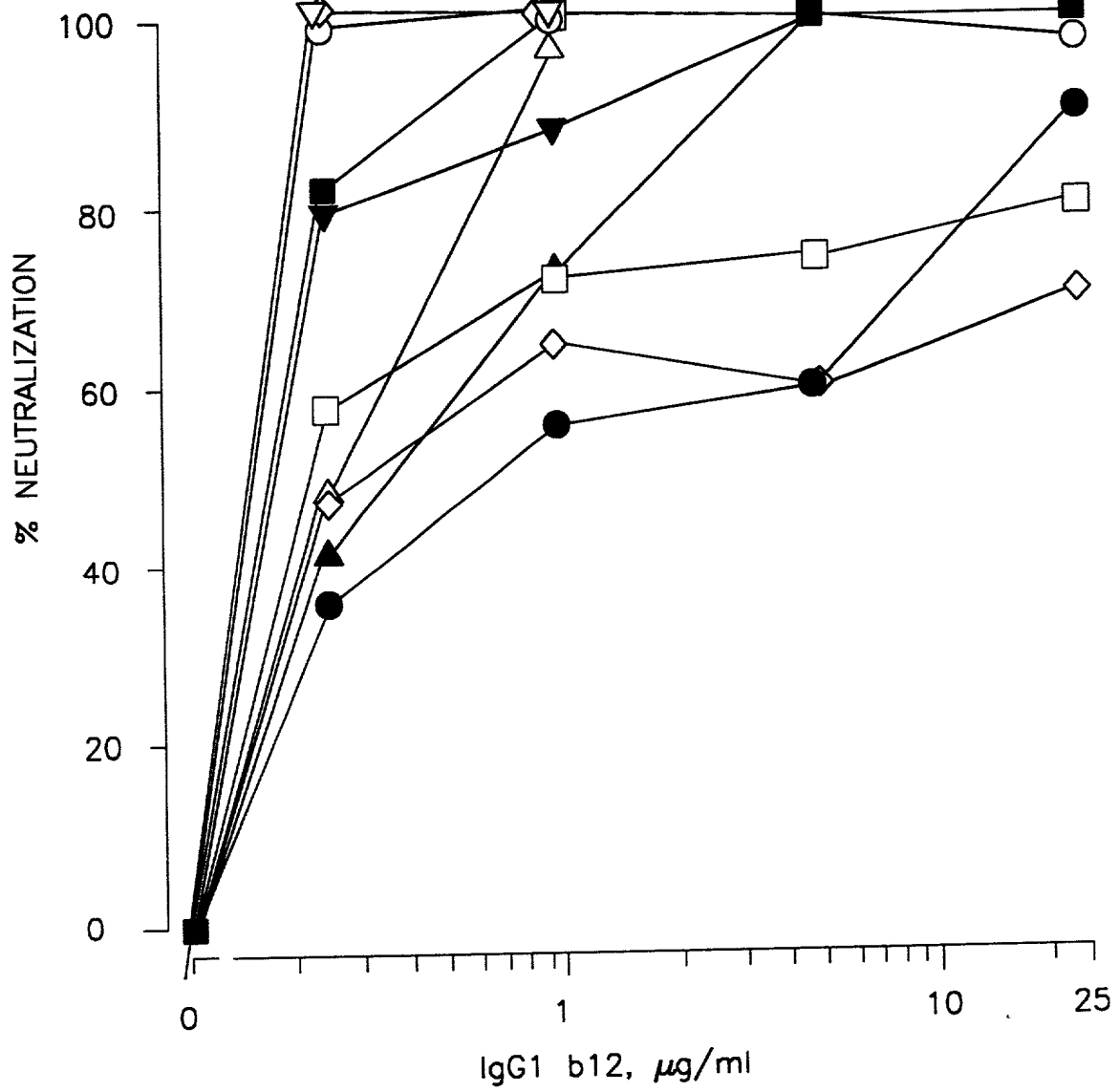


FIG. 21

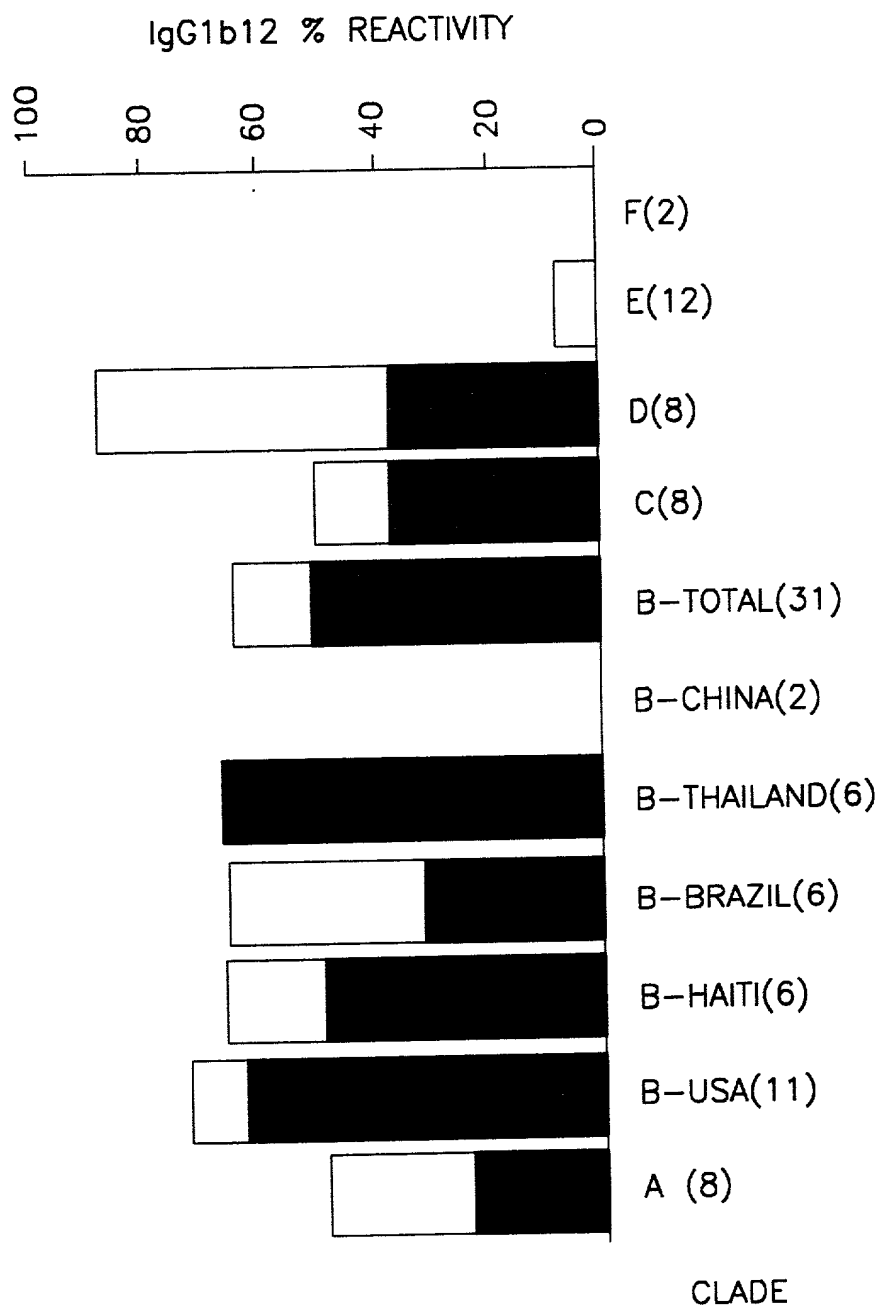


FIG. 22

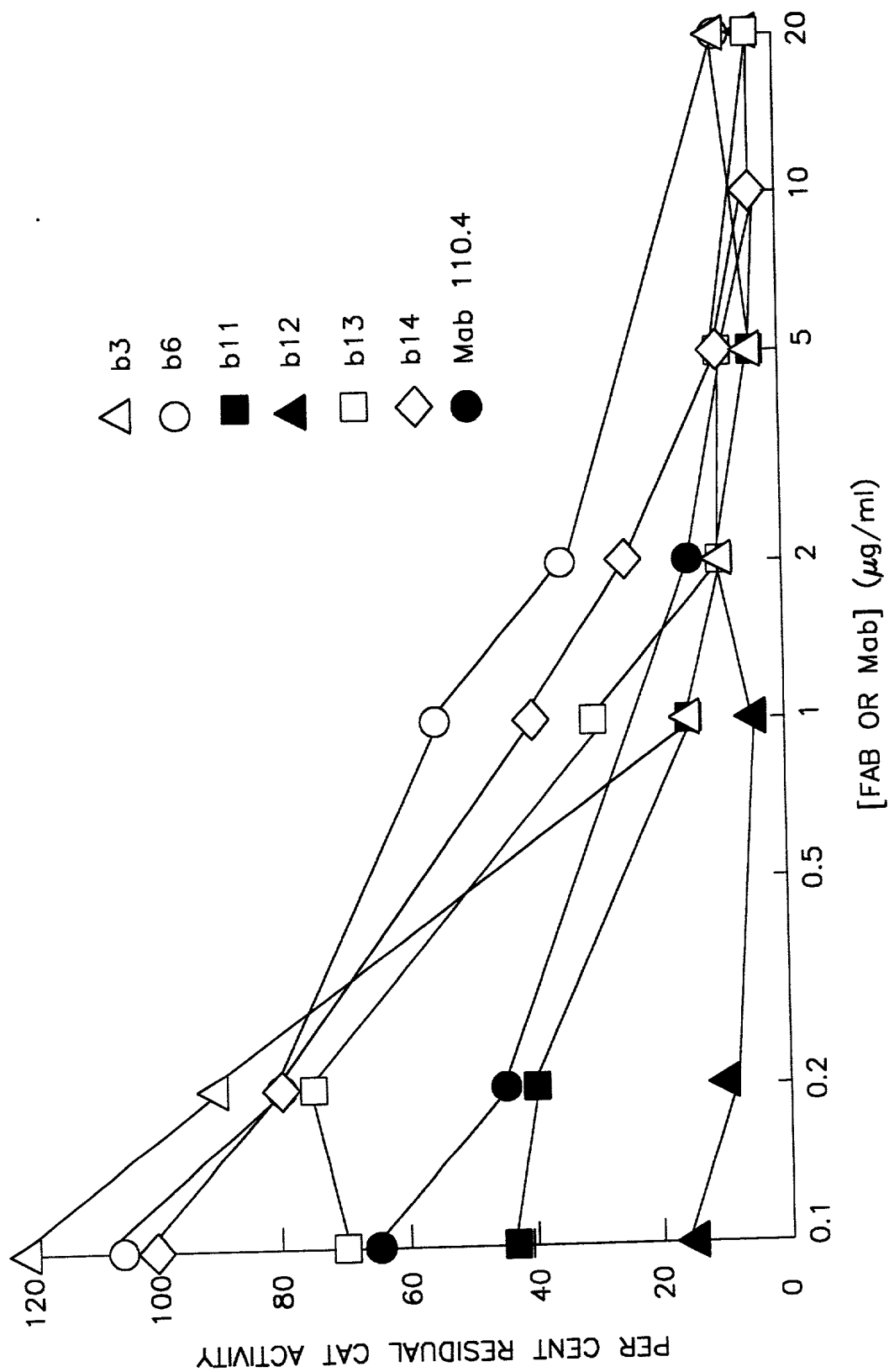


FIG. 23

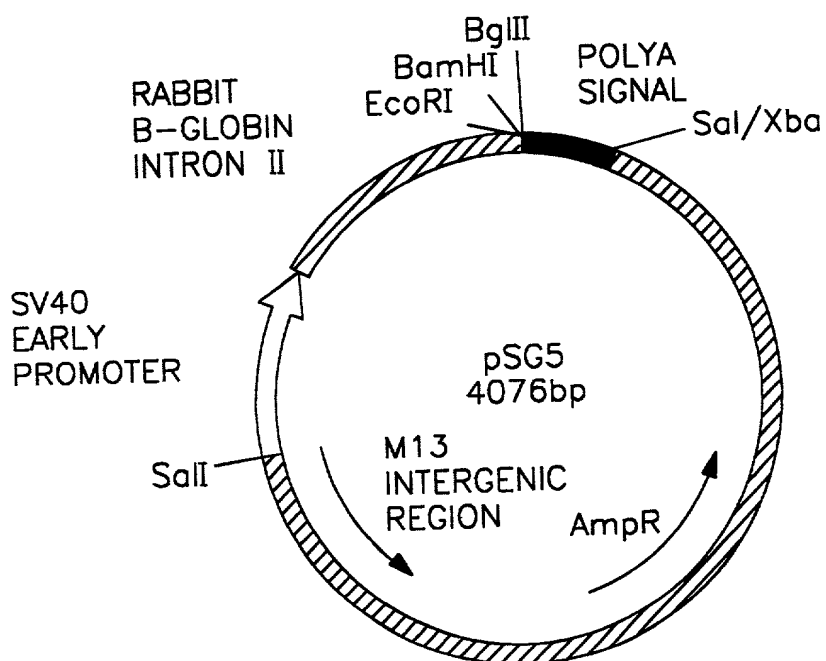


FIG. 24

5	10	15	20	25	30	35	40	45	50	55	60
	*		*		*		*		*		*
AGCTTACCAT	GGGTGTGCCC	ACTCAGGTCC	TGGGGTTGCT	GCTGCTGTGG	CTTACAGATG						
TCGAATGGTA	CCCACACGGG	TGAGTCCAGG	ACCCCAACGA	CGACGACACC	GAATGTCTAC						
	M	G V P	T Q V	L G L L	L L W	L T D					
65	70	75	80	85	90	95	100	105	110	115	120
	*		*		*		*		*		*
CCAGATGTGA	GATCGTTCTC	ACGCAGTCTC	CAGGCACCCT	GTCTCTGTCT	CCAGGGGAAA						
GGTCTACACT	CTAGCAAGAG	TGCGTCAGAG	GTCCGTGGGA	CAGAGACAGA	GGTCCCCTTT						
A R C E	I V L	T Q S	P G T L	S L S	P G E						
125	130	135	140	145	150	155	160	165	170	175	180
	*		*		*		*		*		*
GAGCCACCTT	CTCCTGTAGG	TCCAGTCACA	GCATTTCGCAG	CCGCCGCGTA	GCCTGGTACC						
CTCGGTGGAA	GAGGACATCC	AGGTCAGTGT	CGTAAGCGTC	GGCGGCGCAT	CGGACCATGG						
R A T F	S C R	S S H	S I R S	R R V	A W Y						
185	190	195	200	205	210	215	220	225	230	235	240
	*		*		*		*		*		*
AGCACAAACC	TGGCCAGGCT	CCAAGGCTGG	TCATACATGG	TGTTTCCAAT	AGGGCCTCTG						
TCGTGTTTGG	ACCGGTCCGA	GGTTCGACC	AGTATGTACC	ACAAAGGTTA	TCCCGGAGAC						
Q H K P	G Q A	P R L	V I H G	V S N	R A S						
245	250	255	260	265	270	275	280	285	290	295	300
	*		*		*		*		*		*
GCATCTCAGA	CAGGTTTCAGC	GGCAGTGGGT	CTGGGACAGA	CTTCACTCTC	ACCATCACCA						
CGTAGAGTCT	GTCCAAGTCG	CCGTCACCCA	GACCCTGTCT	GAAGTGAGAG	TGGTAGTGGT						
G I S D	R F S	G S G	S G T D	F T L	T I T						
305	310	315	320	325	330	335	340	345	350	355	360
	*		*		*		*		*		*
GAGTGGAGCC	TGAAGACTTT	GCACTGTACT	ACTGTCAGGT	CTATGGTGCC	TCCTCGTACA						
CTCACCTCGG	ACTTCTGAAA	CGTGACATGA	TGACAGTCCA	GATACCACGG	AGGAGCATGT						
R V E P	E D F	A L Y	Y C Q V	Y G A	S S Y						
365	370	375	380	385	390	395	400	405	410	415	420
	*		*		*		*		*		*
CTTTTGGCCA	GGGGACCAAA	CTGGAGAGGA	AACGAAGTGT	GCCTGCACCA	TCTGTCTTCA						
GGAAACCGGT	CCCCTGGTTT	GACCTCTCCT	TTGCTTGACA	CGGACGTGGT	AGACAGAAGT						
T F G Q	G T K	L E R	K R T V	P A P	S V F						
425	430	435	440	445	450	455	460	465	470	475	480
	*		*		*		*		*		*
TCTTCCCGCC	ATCTGATGAG	CAGTTGAAAT	CTGGGACTGC	CTCTGTTGTG	TGCCTGCTGA						
AGAAGGGCGG	TAGACTACTC	GTCAACTTTA	GACCCTGACG	GAGACAACAC	ACGGACGACT						
I F P P	S D E	Q L K	S G T A	S V V	C L L						
485	490	495	500	505	510	515	520	525	530	535	540
	*		*		*		*		*		*
ATAACTTCTA	TCCCAGAGAG	GCCAAAGTAC	AGTGGAAGGT	GGATAACGCC	CTCCAATCGG						
TATTGAAGAT	AGGGTCTCTC	CGGTTTCATG	TCACCTTCCA	CCTATTGCGG	GAGGTTAGCC						
N N F Y	P R E	A K V	Q W K V	D N A	L Q S						
545	550	555	560	565	570	575	580	585	590	595	600
	*		*		*		*		*		*
GTAAGTCCCA	GGAGAGTGTC	ACAGAGCAGG	ACAGCAAGGA	CAGCACCTAC	AGCCTCAGCA						
CATTGAGGGT	CCTCTCACAG	TGTCTCGTCC	TGTCGTTTCT	GTCTGCGGATG	TCGGAGTCGT						
G N S Q	E S V	T E Q	D S K D	S T Y	S L S						

FIG. 25A

10016986 "10016986"

605	610	615	620	625	630	635	640	645	650	655	660
	*		*		*		*		*		*
GCACCCTGAC	GCTGAGCAAA	GCAGACTACG	AGAAACACAA	AGTCTACGCC	TGCGAAGTCA						
CGTGGGACTG	CGACTCGTTT	CGTCTGATGC	TCTTTGTGTT	TCAGATGCGG	ACGCTTCAGT						
S T L T	L S K	A D Y	E K H K	V Y A	C E V>						
665	670	675	680	685	690	695	700	705	710	715	720
	*		*		*		*		*		*
CCCATCAGGG	CCTGAGTTCG	CCCGTCACAA	AGAGCTTCAA	CAGGGGAGAG	TGTTAATTCT						
GGGTAGTCCC	GGACTCAAGC	GGGCAGTGTT	TCTCGAAGTT	GTCCCCTCTC	ACAATTAAGA						
T H Q G	L S S	P V T	K S F N	R G E	C *>						
725											
AGAGAATTC											
TCTCTTAAG											

FIG. 25B

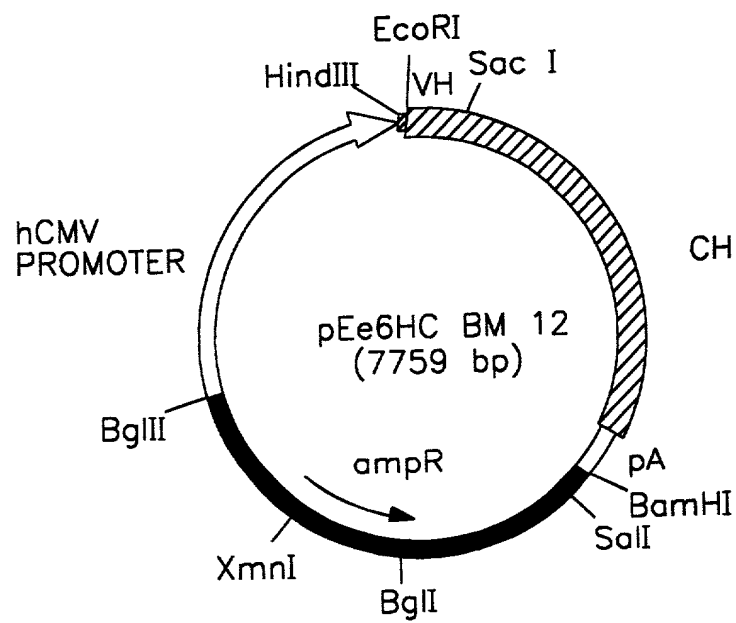


FIG. 26

5	10	15	20	25	30	35	40	45	50	55	60
	*		*		*		*		*		*
AATTCGCCGC	CACCATGGAA	TGGAGCTGGG	TCTTTCTCTT	CTTCCTGTCA	GTAACCTACAG						
TTAAGCGGCG	GTGGTACCTT	ACCTCGACCC	AGAAAGAGAA	GAAGGACAGT	CATTGATGTC						
	M E	W S W	V F L F	F L S	V T T>						
65	70	75	80	85	90	95	100	105	110	115	120
	*		*		*		*		*		*
GTGTCCACTC	CCAGGTTTCA	CTGGTTCAGT	CCGGGGCTGA	GGTGAAGAAG	CCTGGGGCCT						
CACAGGTGAG	GGTCCAAGTC	GACCAAGTCA	GGCCCCGACT	CCACTTCTTC	GGACCCCGGA						
G V H S	Q V Q	L V Q	S G A E	V K K	P G A>						
125	130	135	140	145	150	155	160	165	170	175	180
	*		*		*		*		*		*
CAGTGAAGGT	TTCTTGTCAG	GCTTCTGGAT	ACAGATTCAG	TAACTTTGTT	ATTCATTGGG						
GTCACCTTCCA	AAGAACAGTC	CGAAGACCTA	TGTCTAAGTC	ATTGAAACAA	TAAGTAACCC						
S V K V	S C Q	A S G	Y R F S	N F V	I H W>						
185	190	195	200	205	210	215	220	225	230	235	240
	*		*		*		*		*		*
TGCGCCAGGC	CCCCGGACAG	AGGTTTGAGT	GGATGGGATG	GATCAATCCT	TACAACGGAA						
ACGCGGTCCG	GGGGCCTGTC	TCCAAACTCA	CCTACCCTAC	CTAGTTAGGA	ATGTTGCCTT						
V R Q A	P G Q	R F E	W M G W	I N P	Y N G>						
245	250	255	260	265	270	275	280	285	290	295	300
	*		*		*		*		*		*
ACAAAGAATT	TTCAGCGAAG	TTCCAGGACA	GAGTCACCTT	TACCGCGGAC	ACATCCGCGA						
TGTTTCTTAA	AAGTCGCTTC	AAGGTCCTGT	CTCAGTGGAA	ATGGCGCCTG	TGTAGGCGCT						
N K E F	S A K	F Q D	R V T F	T A D	T S A>						
305	310	315	320	325	330	335	340	345	350	355	360
	*		*		*		*		*		*
ACACAGCCTA	CATGGAGTTG	AGGAGCCTCA	GGTCTGCAGA	CACGGCTGTT	TATTATTGTG						
TGTGTCGGAT	GTACCTCAAC	TCCTCGGAGT	CCAGACGTCT	GTGCCGACAA	ATAATAACAC						
N T A Y	M E L	R S L	R S A D	T A V	Y Y C>						
365	370	375	380	385	390	395	400	405	410	415	420
	*		*		*		*		*		*
CGAGAGTGGG	GCCATATAGT	TGGGATGATT	CTCCCCAGGA	CAATTATTAT	ATGGACGTCT						
GCTCTCACCC	CGGTATATCA	ACCCTACTAA	GAGGGGTCTT	GTTAATAATA	TACCTGCAGA						
A R V G	P Y S	W D D	S P Q D	N Y Y	M D V>						
425	430	435	440	445	450	455	460	465	470	475	480
	*		*		*		*		*		*
GGGGCAAAGG	AACCACGGTC	ATCGTGAGCT	CAGCTTCCAC	CAAGGGCCCCA	TCGGTCTTCC						
CCCCGTTTCC	TTGGTGCCAG	TAGCACTCGA	GTCGAAGGTG	GTTCCCGGGT	AGCCAGAAGG						
W G K G	T T V	I V S	S>								
485	490	495	500	505	510	515	520	525	530	535	540
	*		*		*		*		*		*
CCCTGGCACC	CTCCTCCAAG	AGCACCTCTG	GGGGCACAGC	GGCCCTGGGC	TGCCTGGTCA						
GGGACCGTGG	GAGGAGGTTT	TCGTGGAGAC	CCCCGTGTGG	CCGGGACCCG	ACGGACCACT						
545	550	555	560	565	570	575	580	585	590	595	600
	*		*		*		*		*		*
AGGACTACTT	CCCCGAACCG	GTGACGGTGT	CGTGGAAGTC	AGGCGCCCTG	ACCAGCGGCG						
TCCTGATGAA	GGGGCTTGGC	CACTGCCACA	GCACCTTGAG	TCCGCGGGAC	TGGTCGCGCG						

FIG. 27A

605	610	615	620	625	630	635	640	645	650	655	660
	*		*		*		*		*		*
TGCACACCTT	CCCGGCTGTC	CTACAGTCCT	CAGGACTCTA	CTCCCTCAGC	AGCGTGGTGA						
ACGTGTGGAA	GGGCCGACAG	GATGTCAGGA	GTCCTGAGAT	GAGGGAGTCG	TCGCACCACT						
665	670	675	680	685	690	695	700	705	710	715	720
	*		*		*		*		*		*
CCGTGCCCTC	CAGCAGCTTG	GGCACCCAGA	CCTACATCTG	CAACGTGAAT	CACAAGCCCA						
GGCACGGGAG	GTCGTGGAAC	CCGTGGGTCT	GGATGTAGAC	GTTGCACTTA	GTGTTCCGGT						
725	730	735	740	745	750	755	760	765	770	775	780
	*		*		*		*		*		*
GCAACACCAA	GGTGGACAAG	AAAGTTGGTG	AGAGGCCAGC	ACAGGGAGGG	AGGGTGTCTG						
CGTTGTGGTT	CCACCTGTTC	TTTCAACCAC	TCTCCGGTCG	TGTCCCTCCC	TCCCACAGAC						
785	790	795	800	805	810	815	820	825	830	835	840
	*		*		*		*		*		*
CTGGAAGCCA	GGCTCAGCGC	TCCTGCCTGG	ACGCATCCCG	GCTATGCAGC	CCCAGTCCAG						
GACCTTCGGT	CCGAGTCGCG	AGGACGGACC	TGCGTAGGGC	CGATACGTCG	GGGTGAGGTC						
845	850	855	860	865	870	875	880	885	890	895	900
	*		*		*		*		*		*
GGCAGCAAGG	CAGGCCCCGT	CTGCCTCTTC	ACCCGGAGGC	CTCTGCCCGC	CCCACTCATG						
CCGTGCTTCC	GTCCGGGGCA	GACGGAGAAG	TGGGCCTCCG	GAGACGGGCG	GGGTGAGTAC						
905	910	915	920	925	930	935	940	945	950	955	960
	*		*		*		*		*		*
CTCAGGGAGA	GGGTCTTCTG	GCTTTTTCCC	CAGGCTCTGG	GCAGGCACAG	GCTAGGTGCC						
GAGTCCCTCT	CCCAGAAGAC	CGAAAAAGGG	GTCCGAGACC	CGTCCGTGTC	CGATCCACGG						
965	970	975	980	985	990	995	1000	1005	1010	1015	1020
	*		*		*		*		*		*
CCTAACCAG	GCCCTGCACA	CAAAGGGGCA	GGTGTGGGTC	TCAGACCTGC	CAAGAGCCAT						
GGATTGGGTC	CGGGACGTGT	GTTTCCCCGT	CCACGACCCG	AGTCTGGACG	GTTCTCGGTA						
1025	1030	1035	1040	1045	1050	1055	1060	1065	1070	1075	1080
	*		*		*		*		*		*
ATCCGGGAGG	ACCCTGCCCC	TGACCTAAGC	CCACCCCAAA	GGCCAAACTC	TCCACTCCCT						
TAGGCCCTCC	TGGGACGGGG	ACTGGATTCTG	GGTGGGGTTT	CCGGTTTGAG	AGGTGAGGGA						
1085	1090	1095	1100	1105	1110	1115	1120	1125	1130	1135	1140
	*		*		*		*		*		*
CAGCTCGGAC	ACCTTCTCTC	CTCCCAGATT	CGAGTAACTC	CCAATCTTCT	CTCTGCAGAG						
GTCGAGCCTG	TGGAAGAGAG	GAGGGTCTAA	GCTCATTGAG	GGTTAGAAGA	GAGACGTCTC						
1145	1150	1155	1160	1165	1170	1175	1180	1185	1190	1195	1200
	*		*		*		*		*		*
CCCAAATCTT	GTGACAAAAC	TCACACATGC	CCACCGTGCC	CAGGTAAGCC	AGCCCAGGCC						
GGGTTTAGAA	CACTGTTTTG	AGTGTGTACG	GGTGGCACGG	GTCCATTCCG	TGGGGTCCGG						
1205	1210	1215	1220	1225	1230	1235	1240	1245	1250	1255	1260
	*		*		*		*		*		*
TCGCCCTCCA	GCTCAAGGCG	GGACAGGTGC	CCTAGAGTAG	CCTGCATCCA	GGGACAGGCC						
AGCGGGAGGT	CGAGTTCCGC	CCTGTCCACG	GGATCTCATC	GGACGTAGGT	CCCTGTCCGG						
1265	1270	1275	1280	1285	1290	1295	1300	1305	1310	1315	1320
	*		*		*		*		*		*
CCAGCCGGGT	GCTGACACGT	CCACCTCCAT	CTCTCCCTCA	GCACCTGAGG	CCGCGGGAGG						
GGTCGGCCCA	CGACTGTGCA	GGTGGAGGTA	GAGAGGGAGT	CGTGGACTCC	GGCGCCCTCC						

FIG. 27B

1325 1330	1335 1340	1345 1350	1355 1360	1365 1370	1375 1380
* *	* *	* *	* *	* *	* *
ACCATCAGTC	TTCCTCTTCC	CCCCAAAACC	CAAGGACACC	CTCATGATCT	CCCGGACCCC
TGGTAGTCAG	AAGGAGAAGG	GGGGTTTTTG	GTTCTGTGG	GAGTACTAGA	GGGCCTGGGG
1385 1390	1395 1400	1405 1410	1415 1420	1425 1430	1435 1440
* *	* *	* *	* *	* *	* *
TGAGGTCACA	TGCGTGGTGG	TGGACGTGAG	CCACGAAGAC	CCTGAGGTCA	AGTTCAACTG
ACTCCAGTGT	ACGCACCACC	ACCTGCACTC	GGTGCTTCTG	GGACTCCAGT	TCAAGTTGAC
1445 1450	1455 1460	1465 1470	1475 1480	1485 1490	1495 1500
* *	* *	* *	* *	* *	* *
GTACGTGGAC	GGCGTGGAGG	TGCATAATGC	CAAGACAAAG	CCGCGGGAGG	AGCAGTACAA
CATGCACCTG	CCGCACCTCC	ACGTATTACG	GTTCTGTTTC	GGCGCCCTCC	TCGTCATGTT
1505 1510	1515 1520	1525 1530	1535 1540	1545 1550	1555 1560
* *	* *	* *	* *	* *	* *
CAGCACGTAC	CGTGTGGTCA	GCGTCCTCAC	CGTCCTGCAC	CAGGACTGGC	TGAATGGCAA
GTCGTGCATG	GCACACCAGT	CGCAGGAGTG	GCAGGACGTG	GTCCTGACCG	ACTTACCGTT
1565 1570	1575 1580	1585 1590	1595 1600	1605 1610	1615 1620
* *	* *	* *	* *	* *	* *
GGAGTACAAG	TGCAAGGTCT	CCAACAAAGC	CCTCCCAGCC	CCCATCGAGA	AAACCATCTC
CCTCATGTTC	ACGTTCCAGA	GGTGTGTTTC	GGAGGGTCGG	GGGTAGCTCT	TTTGGTAGAG
1625 1630	1635 1640	1645 1650	1655 1660	1665 1670	1675 1680
* *	* *	* *	* *	* *	* *
CAAAGCCAAA	GGTGGGACCC	GTGGGGTGCG	AGGGCCACAT	GGACAGAGGC	CGGCTCGGCC
GTTTCGGTTT	CCACCCTGGG	CACCCCACGC	TCCCCGGTGA	CCTGTCTCCG	GCCGAGCCGG
1685 1690	1695 1700	1705 1710	1715 1720	1725 1730	1735 1740
* *	* *	* *	* *	* *	* *
CACCCTCTGC	CCTGAGAGTG	ACCGCTGTAC	CAACCTCTGT	CCCTACAGGG	CAGCCCCGAG
GTGGGAGACG	GGACTCTCAC	TGGCGACATG	GTTGGAGACA	GGGATGTCCC	GTCGGGGCTC
1745 1750	1755 1760	1765 1770	1775 1780	1785 1790	1795 1800
* *	* *	* *	* *	* *	* *
AACCACAGGT	GTACACCCTG	CCCCCATCCC	GGGATGAGCT	GACCAAGAAC	CAGGTCAGCC
TTGGTGTCCA	CATGTGGGAC	GGGGGTAGGG	CCCTACTCGA	CTGGTTCTTG	GTCCAGTCGG
1805 1810	1815 1820	1825 1830	1835 1840	1845 1850	1855 1860
* *	* *	* *	* *	* *	* *
TGACCTGCCT	GGTCAAAGGC	TTCTATCCCA	GCGACATCGC	CGTGGAGTGG	GAGAGCAATG
ACTGGACGGA	CCAGTTTCCG	AAGATAGGGT	CGCTGTAGCG	GCACCTCACC	CTCTCGTTAC
1865 1870	1875 1880	1885 1890	1895 1900	1905 1910	1915 1920
* *	* *	* *	* *	* *	* *
GGCAGCCGGA	GAACAACTAC	AAGACCACGC	CTCCCGTGCT	GGACTCCGAC	GGCTCCTTCT
CCGTGCGCCT	CTTGTTGATG	TTCTGGTGCG	GAGGGCACGA	CCTGAGGCTG	CCGAGGAAGA
1925 1930	1935 1940	1945 1950	1955 1960	1965 1970	1975 1980
* *	* *	* *	* *	* *	* *
TCCTCTACAG	CAAGCTCACC	GTGGACAAGA	GCAGGTGGCA	GCAGGGGAAC	GTCTTCTCAT
AGGAGATGTC	GTTTCGAGTG	CACCTGTTCT	CGTCCACCGT	CGTCCCCTTG	CAGAAGAGTA
1985 1990	1995 2000	2005 2010	2015 2020	2025 2030	2035 2040
* *	* *	* *	* *	* *	* *
GCTCCGTGAT	GATGAGGCT	CTGCACAACC	ACTACACGCA	GAAGAGCCTC	TCCCTGTCTC
CGAGGCACTA	CGTACTCCGA	GACGTGTTGG	TGATGTGCGT	CTTCTCGGAG	AGGGACAGAG

FIG. 27C

2045	2050	2055	2060	2065	2070	2075	2080	2085	2090	2095	2100
	*		*		*		*		*		*
CGGGTAAATG	AGTGCGACGG	CCGGCAAGCC	CCCGCTCCCC	GGCGCTCCCG	GGCGGAGGGG	GGGCTCTCGC	GGGCTCTCGC	GGGCTCTCGC	GGGCTCTCGC	GGTGCACGA	GGTGCACGA
GCCCATTTAC	TCACGCTGCC	GGCCGTTCCG	GGCGCTCCCG	GGCGGAGGGG	GGGCTCTCGC	GGGCTCTCGC	GGGCTCTCGC	GGGCTCTCGC	GGGCTCTCGC	GGTGCACGA	GGTGCACGA
2105	2110	2115	2120	2125	2130	2135	2140	2145	2150	2155	2160
	*		*		*		*		*		*
GGATGCTTGG	CACGTACCCC	CTGTACATAC	TTCCCGGGCG	CCCAGCATGG	AAATAAAGCA	GGATGCTTGG	CACGTACCCC	CTGTACATAC	TTCCCGGGCG	CCCAGCATGG	AAATAAAGCA
CCTACGAACC	GTGCATGGGG	GACATGTATG	AAGGGCCCCG	GGGTCGTACC	TTTATTTTCGT	GGATGCTTGG	CACGTACCCC	CTGTACATAC	TTCCCGGGCG	CCCAGCATGG	AAATAAAGCA
2165	2170	2175	2180	2185	2190	2195	2200	2205	2210	2215	2220
	*		*		*		*		*		*
CCCAGCGCTG	CCCTGGGCCC	CTGCGAGACT	GTGATGGTTC	TTTCCACGGG	TCAGGCCGAG	CCCAGCGCTG	CCCTGGGCCC	CTGCGAGACT	GTGATGGTTC	TTTCCACGGG	TCAGGCCGAG
GGGTCGCGAC	GGGACCCGGG	GACGCTCTGA	CACTACCAAG	AAAGGTGCCC	AGTCCGGCTC	CCCAGCGCTG	CCCTGGGCCC	CTGCGAGACT	GTGATGGTTC	TTTCCACGGG	TCAGGCCGAG
2225	2230	2235	2240	2245	2250	2255	2260	2265	2270	2275	2280
	*		*		*		*		*		*
TCTGAGGCCT	GAGTGGCATG	AGGGAGGCAG	AGCGGGTCCC	ACTGTCCCCA	CACTGGCCCA	TCTGAGGCCT	GAGTGGCATG	AGGGAGGCAG	AGCGGGTCCC	ACTGTCCCCA	CACTGGCCCA
AGACTCCGGA	CTCACCCTAC	TCCCTCCGTC	TGCCCCAGGG	TGACAGGGGT	GTGACCCGGT	TCTGAGGCCT	GAGTGGCATG	AGGGAGGCAG	AGCGGGTCCC	ACTGTCCCCA	CACTGGCCCA
2285	2290	2295	2300	2305	2310	2315	2320	2325	2330	2335	2340
	*		*		*		*		*		*
GGCTGTGCAG	GTGTGCCTGG	GCCGCCTAGG	GTGGGGCTCA	GCCAGGGGCT	GCCCTCGGCA	GGCTGTGCAG	GTGTGCCTGG	GCCGCCTAGG	GTGGGGCTCA	GCCAGGGGCT	GCCCTCGGCA
CCGACACGTC	CACACGGACC	CGGCGGATCC	CACCCCGAGT	CGGTCCCCGA	CGGGAGCCGT	GGCTGTGCAG	GTGTGCCTGG	GCCGCCTAGG	GTGGGGCTCA	GCCAGGGGCT	GCCCTCGGCA
2345	2350	2355	2360	2365	2370	2375	2380	2385	2390	2395	2400
	*		*		*		*		*		*
GGGTGGGGGA	TTTGCCAGCG	TTGCCCTCCC	TCCAGCAGCA	CCTGCCCTGG	GCTGGGCCAC	GGGTGGGGGA	TTTGCCAGCG	TTGCCCTCCC	TCCAGCAGCA	CCTGCCCTGG	GCTGGGCCAC
CCCACCCCT	AAACGGTCGC	AACGGGAGGG	AGGTCGTCGT	GGACGGGACC	CGACCCGGTG	GGGTGGGGGA	TTTGCCAGCG	TTGCCCTCCC	TCCAGCAGCA	CCTGCCCTGG	GCTGGGCCAC
2405	2410	2415	2420	2425	2430	2435	2440	2445	2450	2455	2460
	*		*		*		*		*		*
GGGAAGCCCT	AGGAGCCCT	GGGGACAGAC	ACACAGCCCC	TGCCTCTGTA	GGAGACTGTC	GGGAAGCCCT	AGGAGCCCT	GGGGACAGAC	ACACAGCCCC	TGCCTCTGTA	GGAGACTGTC
CCCTTCGGGA	TCCTCGGGGA	CCCCTGTCTG	TGTGTGCGGG	ACGGAGACAT	CCTCTGACAG	GGGAAGCCCT	AGGAGCCCT	GGGGACAGAC	ACACAGCCCC	TGCCTCTGTA	GGAGACTGTC
2465	2470	2475	2480	2485	2490	2495	2500	2505	2510	2515	2520
	*		*		*		*		*		*
CTGTTCTGTG	AGCGCCCTGT	CCTCCGACCT	CCATGCCCAC	TCGGGGGCAT	GCCTAGTCCA	CTGTTCTGTG	AGCGCCCTGT	CCTCCGACCT	CCATGCCCAC	TCGGGGGCAT	GCCTAGTCCA
GACAAGACAC	TCGCGGGACA	GGAGGCTGGA	GGTACGGGTG	AGCCCCCGTA	CGGATCAGGT	GACAAGACAC	TCGCGGGACA	GGAGGCTGGA	GGTACGGGTG	AGCCCCCGTA	CGGATCAGGT
2525	2530	2535	2540	2545	2550	2555	2560	2565	2570	2575	2580
	*		*		*		*		*		*
TGTGCGTAGG	GACAGGCCCT	CCCTCACCCA	TCTACCCCCA	CGGCACTAAC	CCCTGGCTGT	TGTGCGTAGG	GACAGGCCCT	CCCTCACCCA	TCTACCCCCA	CGGCACTAAC	CCCTGGCTGT
ACACGCATCC	CTGTCCGGGA	GGGAGTGGGT	AGATGGGGGT	GCCGTGATTG	GGGACCGACA	TGTGCGTAGG	GACAGGCCCT	CCCTCACCCA	TCTACCCCCA	CGGCACTAAC	CCCTGGCTGT
2585	2590	2595	2600	2605	2610	2615	2620	2625	2630	2635	2640
	*		*		*		*		*		*
CCTGCCCAGC	CTCGCACCCG	CATGGGGACA	CAACCGACTC	CGGGGACATG	CACTCTCGGG	CCTGCCCAGC	CTCGCACCCG	CATGGGGACA	CAACCGACTC	CGGGGACATG	CACTCTCGGG
GGACGGGTG	GAGCGTGGGC	GTACCCCTGT	GTTGGCTGAG	GCCCCTGTAC	GTGAGAGCCC	GGACGGGTG	GAGCGTGGGC	GTACCCCTGT	GTTGGCTGAG	GCCCCTGTAC	GTGAGAGCCC
2645	2650	2655	2660	2665	2670	2675	2680	2685	2690	2695	2700
	*		*		*		*		*		*
CCCTGTGGAG	GGACTGGTGC	AGATGCCCAC	ACACACACTC	AGTCCAGACC	CGTTCAACAA	CCCTGTGGAG	GGACTGGTGC	AGATGCCCAC	ACACACACTC	AGTCCAGACC	CGTTCAACAA
GGGACACCTC	CCTGACCACG	TCTACGGGTG	TGTGTGTGAG	TCAGGTCTGG	GCAAGTTGTT	GGGACACCTC	CCTGACCACG	TCTACGGGTG	TGTGTGTGAG	TCAGGTCTGG	GCAAGTTGTT
2705	2710	2715	2720	2725	2730	2735	2740	2745	2750	2755	2760
	*		*		*		*		*		*
AACCCCCGCA	CTGAGGTTGG	CCGGCCACAC	GGCCACCACA	CACACACGTG	CACGCCTCAC	AACCCCCGCA	CTGAGGTTGG	CCGGCCACAC	GGCCACCACA	CACACACGTG	CACGCCTCAC
TTGGGGGCGT	GACTCCAACC	GGCCGGTGTG	CCGGTGGTGT	GTGTGTGCAC	GTGCGGAGTG	TTGGGGGCGT	GACTCCAACC	GGCCGGTGTG	CCGGTGGTGT	GTGTGTGCAC	GTGCGGAGTG

FIG. 27D

2765	2770	2775	2780	2785	2790	2795	2800	2805	2810	2815	2820
	*		*		*		*		*		*
ACACGGAGCC	TCACCCGGGC	GAACCTGCACA	GCACCCAGAC	CAGAGCAAGG	TCCTCGCACA	TGTGCCTCGG	AGTGGGCCCC	CTTGACGTGT	CGTGGGTCTG	GTCTCGTTCC	AGGAGCGTGT
2825	2830	2835	2840	2845	2850	2855	2860	2865	2870	2875	2880
	*		*		*		*		*		*
CGTGAACACT	CCTCGGACAC	AGGCCCCAC	GAGCCCCACG	CGGCACCTCA	AGGCCACGA	GCACTTGTGA	GGAGCCTGTG	TCCGGGGGTG	CTCGGGGTGC	GCCGTGGAGT	TCCGGGTGCT
2885	2890	2895	2900	2905	2910	2915	2920	2925	2930	2935	2940
	*		*		*		*		*		*
GCCTCTCGGC	AGCTTCTCCA	CATGCTGACC	TGCTCAGACA	AACCCAGCCC	TCCTCTCACA	CGGAGAGCCG	TCGAAGAGGT	GTACGACTGG	ACGAGTCTGT	TTGGGTCCGG	AGGAGAGTGT
2945	2950	2955	2960	2965	2970	2975	2980	2985	2990	2995	3000
	*		*		*		*		*		*
AGGGTGCCCC	TGCAGCCGCC	ACACACACAC	AGGGGATCAC	ACACCACGTC	ACGTCCCTGG	TCCCACGGGG	ACGTCCGGCG	TGTGTGTGTG	TCCCCTAGTG	TGTGGTGCAG	TGCAGGGACC
3005	3010	3015	3020	3025	3030	3035	3040	3045	3050	3055	3060
	*		*		*		*		*		*
CCCTGGCCCA	CTTCCCAGTG	CCGCCCTTCC	CTGCAGGGCG	GATCATAATC	AGCCATACCA	GGGACCGGGT	GAAGGGTCAC	GGCGGGAAGG	GACGTCCCGC	CTAGTATTAG	TGGGTATGGT
3065	3070	3075	3080	3085	3090	3095	3100	3105	3110	3115	3120
	*		*		*		*		*		*
CATTTGTAGA	GGTTTTACTT	GCTTTAAAAA	ACCTCCCACA	CCTCCCCCTG	AACCTGAAAC	GTAAACATCT	CCAAAATGAA	CGAAATTTTT	TGGAGGGTGT	GGAGGGGGAC	TTGGACTTTG
3125	3130	3135	3140	3145	3150	3155	3160	3165	3170	3175	3180
	*		*		*		*		*		*
ATAAAATGAA	TGCAATTGTT	GTTGTTAACT	TGTTTATTGC	AGCTTATAAT	GGTTACAAAT	TATTTTACTT	ACGTTAACAA	CAACAATTGA	ACAAATAACG	TCAATATTA	CCAATGTTTA
3185	3190	3195	3200	3205	3210	3215	3220	3225	3230	3235	3240
	*		*		*		*		*		*
AAAGCAATAG	CATCACAAAT	TTCACAAATA	AAGCATTTTT	TTCAGTGCAT	TCTAGTTGTG	TTTCGTTATC	GTAGTGTTTA	AAGTGTTTAT	TTCGTAAAAA	AAGTGACGTA	AGATCAACAC
3245	3250	3255	3260	3265	3270	3275	3280				
	*		*		*		*				
GTTTGTCCAA	ACTCATCAAT	GTATCTTATC	ATGTCTAGAT	CC		CAAACAGGTT	TGAGTAGTTA	CATAGAATAG	TACAGATCTA	GG	

FIG. 27E

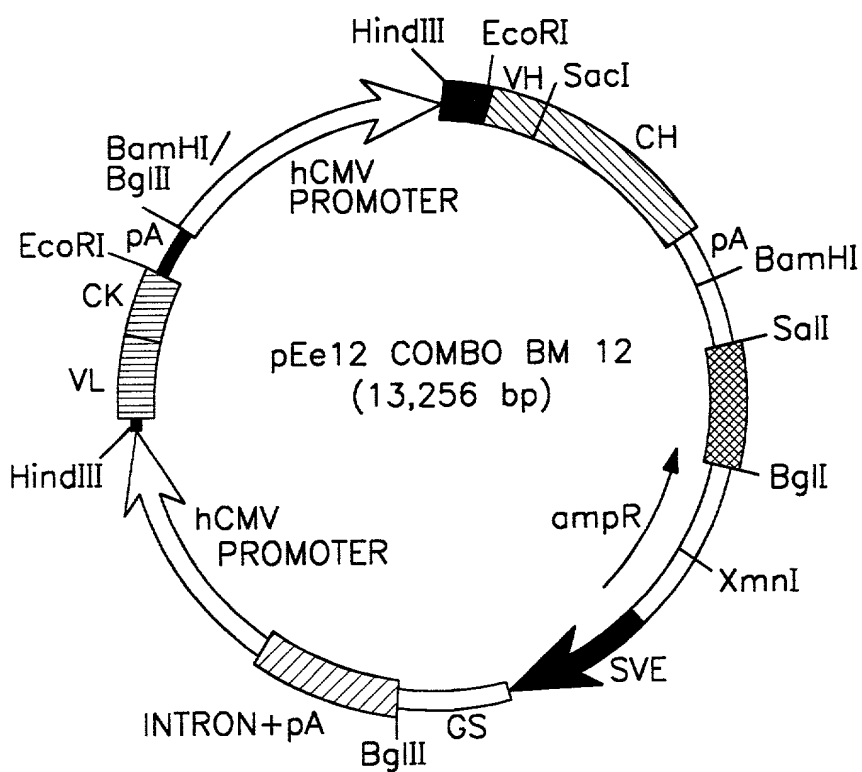


FIG. 28

5	10	15	20	25	30	35	40	45	50	55	60
	*		*		*		*		*		*
TTCATTGATC	ATTAATCAGC	CATACCACAT	TTGTAGAGGT	TTTACTTGCT	TTAAAAAACC						
AAGTAACTAG	TAATTAGTCG	GTATGGTGTA	AACATCTCCA	AAATGAACGA	AATTTTTTTG						
65	70	75	80	85	90	95	100	105	110	115	120
	*		*		*		*		*		*
TCCACACCT	CCCCCTGAAC	CTGAAACATA	AAATGAATGC	AATTGTTGTT	GTAACTTGT						
AGGGTGTGGA	GGGGGACTTG	GACTTTGTAT	TTTACTTACG	TTAACAACAA	CAATTGAACA						
125	130	135	140	145	150	155	160	165	170	175	180
	*		*		*		*		*		*
TTATTGCAGC	TTATAATGGT	TACAAATAAA	GCAATAGCAT	CACAAATTTT	ACAAATAAAG						
AATAACGTCG	AATATTACCA	ATGTTTATTT	CGTTATCGTA	GTGTTTAAAG	TGTTTATTTT						
185	190	195	200	205	210	215	220	225	230	235	240
	*		*		*		*		*		*
CATTTTTTTT	ACTGCATTCT	AGTTGTGGTT	TGTCCAAACT	CATCAATGTA	TCTTATCATG						
GTAAAAAAG	TGACGTAAGA	TCAACACCAA	ACAGGTTTGA	GTAGTTACAT	AGAATAGTAC						
245	250	255	260	265	270	275	280	285	290	295	300
	*		*		*		*		*		*
TCTGGATCTC	TAGCTTCGTG	TCAAGGACGG	TGACTGCAGT	GAATAATAAA	ATGTGTGTTT						
AGACCTAGAG	ATCGAAGCAC	AGTTCCTGCC	ACTGACGTCA	CTTATTATTT	TACACACAAA						
305	310	315	320	325	330	335	340	345	350	355	360
	*		*		*		*		*		*
GTCCGAAATA	CGCGTTTTGA	GATTTCTGTC	GCCGACTAAA	TTCATGTGCG	GCGATAGTGG						
CAGGCTTTAT	GCGCAAAACT	CTAAAGACAG	CGGCTGATTT	AAGTACAGCG	CGCTATCACC						
365	370	375	380	385	390	395	400	405	410	415	420
	*		*		*		*		*		*
TGTTTATCGC	CGATAGAGAT	GGCGATATTG	GAAAAATCGA	TATTTGAAAA	TATGGCATAT						
ACAAATAGCG	GCTATCTCTA	CCGCTATAAC	CTTTTTAGCT	ATAAACTTTT	ATACCGTATA						
425	430	435	440	445	450	455	460	465	470	475	480
	*		*		*		*		*		*
TGAAAATGTC	GCCGATGTGA	GTTTCTGTGT	AACTGATATC	GCCATTTTTT	CAAAAGTGAT						
ACTTTTACAG	CGGCTACACT	CAAAGACACA	TTGACTATAG	GCCTAAAAAG	GTTTTCACTA						
485	490	495	500	505	510	515	520	525	530	535	540
	*		*		*		*		*		*
TTTTGGGCAT	ACGCGATATC	TGGCGATAGC	GCTTATATCG	TTTACGGGGG	ATGGCGATAG						
AAAACCCGTA	TGCGCTATAG	ACCGCTATCG	CGAATATAGC	AAATGCCCCC	TACCGCTATC						
545	550	555	560	565	570	575	580	585	590	595	600
	*		*		*		*		*		*
ACGACTTTGG	TGACTTGGGC	GATTCTGTGT	GTCGCAAATA	TCGCAGTTTC	GATATAGGTG						
TGCTGAAACC	ACTGAACCCG	CTAAGACACA	CAGCGTTTAT	AGCGTCAAAG	CTATATCCAC						
605	610	615	620	625	630	635	640	645	650	655	660
	*		*		*		*		*		*
ACAGACGATA	TGAGGCTATA	TCGCCGATAG	AGGCGACATC	AAGCTGGCAC	ATGGCCAATG						
TGTCTGCTAT	ACTCCGATAT	AGCGGCTATC	TCCGCTGTAG	TTCCGACCGT	TACCGGTTAC						
665	670	675	680	685	690	695	700	705	710	715	720
	*		*		*		*		*		*
CATATCGATC	TATACATTGA	ATCAATATTG	GCCATTAGCC	ATATTATTCA	TTGGTTATAT						
GTATAGCTAG	ATATGTAACT	TAGTTATAAC	CGGTAATCGG	TATAATAAGT	AACCAATATA						

FIG. 29A

725	730	735	740	745	750	755	760	765	770	775	780
	*		*		*		*		*		*
AGCATAAATC	AATATTGGCT	ATTGGCCATT	GCATACGTTG	TATCCATATC	ATAATATGTA						
TCGTATTTAG	TTATAACCGA	TAACCGGTAA	CGTATGCAAC	ATAGGTATAG	TATTATACAT						
785	790	795	800	805	810	815	820	825	830	835	840
	*		*		*		*		*		*
CATTTATATT	GGCTCATGTC	CAACATTACC	GCCATGTTGA	CATTGATTAT	TGACTAGTTA						
GTAAATATAA	CCGAGTACAG	GTTGTAATGG	CGGTACAAC	GTAACATAA	ACTGATCAAT						
845	850	855	860	865	870	875	880	885	890	895	900
	*		*		*		*		*		*
TTAATAGTAA	TCAATTACGG	GGTCATTAGT	TCATAGCCCA	TATATGGAGT	TCCGCGTTAC						
AATTATCATT	AGTTAATGCC	CCAGTAATCA	AGTATCGGGT	ATATACCTCA	AGGCGCAATG						
905	910	915	920	925	930	935	940	945	950	955	960
	*		*		*		*		*		*
ATAACTTACG	GTAAATGGCC	CGCCTGGCTG	ACCGCCCAAC	GACCCCCGCC	CATTGACGTC						
TATTGAATGC	CATTTACCGG	GCGGACCGAC	TGGCGGGTTG	CTGGGGGCGG	GTAACCTGCAG						
965	970	975	980	985	990	995	1000	1005	1010	1015	1020
	*		*		*		*		*		*
AATAATGACG	TATGTTCCCA	TAGTAACGCC	AATAGGGACT	TTCCATTGAC	GTCAATGGGT						
TTATTACTGC	ATACAAGGGT	ATCATTGCGG	TTATCCCTGA	AAGGTAACCTG	CAGTTACCCA						
1025	1030	1035	1040	1045	1050	1055	1060	1065	1070	1075	1080
	*		*		*		*		*		*
GGAGTATTTA	CGGTAAACTG	CCCACTTGGC	AGTACATCAA	GTGTATCATA	TGCCAAGTAC						
CCTCATAAAT	GCCATTTGAC	GGGTGAACCG	TCATGTAGTT	CACATAGTAT	ACGGTTCATG						
1085	1090	1095	1100	1105	1110	1115	1120	1125	1130	1135	1140
	*		*		*		*		*		*
GCCCCCTATT	GACGTCAATG	ACGGTAAATG	GCCCGCCTGG	CATTATGCCC	AGTACATGAC						
CGGGGGATAA	CTGCAGTTAC	TGCCATTTAC	CGGGCGGACC	GTAATACGGG	TCATGTACTG						
1145	1150	1155	1160	1165	1170	1175	1180	1185	1190	1195	1200
	*		*		*		*		*		*
CTTATGGGAC	TTTCCTACTT	GGCAGTACAT	CTACGTATTA	GTCATCGCTA	TTACCATGGT						
GAATACCCTG	AAAGGATGAA	CCGTCATGTA	GATGCATAAT	CAGTAGCGAT	AATGGTACCA						
1205	1210	1215	1220	1225	1230	1235	1240	1245	1250	1255	1260
	*		*		*		*		*		*
GATGCGGTTT	TGGCAGTACA	TCAATGGGCG	TGGATAGCGG	TTTGACTCAC	GGGGATTTC						
CTACGCCAAA	ACCGTCATGT	AGTTACCCGC	ACCTATCGCC	AAACTGAGTG	CCCCTAAAGG						
1265	1270	1275	1280	1285	1290	1295	1300	1305	1310	1315	1320
	*		*		*		*		*		*
AAGTCTCCAC	CCCATTGACG	TCAATGGGAG	TTTGTTTTGG	CACCAAAATC	AACGGGACTT						
TTCAGAGGTG	GGGTAACTGC	AGTTACCCCTC	AAACAAAACC	GTGGTTTTAG	TTGCCCTGAA						
1325	1330	1335	1340	1345	1350	1355	1360	1365	1370	1375	1380
	*		*		*		*		*		*
TCCAAAATGT	CGTAACAAC	CCGCCCCATT	GACGCAAATG	GGCGGTAGGC	GTGTACGGTG						
AGGTTTTTACA	GCATTGTTGA	GGCGGGGTAA	CTGCGTTTAC	CCGCCATCCG	CACATGCCAC						
1385	1390	1395	1400	1405	1410	1415	1420	1425	1430	1435	1440
	*		*		*		*		*		*
GGAGGTCTAT	ATAAGCAGAG	CTCGTTTAGT	GAACCGTCAG	ATCGCCTGGA	GACGCCATCC						
CCTCCAGATA	TATTCGTCTC	GAGCAAATCA	CTTGGCAGTC	TAGCGGACCT	CTGCGGTAGG						

FIG. 29B

1445 1450 * ACGCTGTTTT TGCGACAAAA	1455 1460 * GACCTCCATA CTGGAGGTAT	1465 1470 * GAAGACACCG CTTCTGTGGC	1475 1480 * GGACCGATCC CCTGGCTAGG	1485 1490 * AGCCTCCGCG TCGGAGGCGC	1495 1500 * GCCGGGAACG CGGCCCTTGC
1505 1510 * GTGCATTGGA CACGTAACCT	1515 1520 * ACGCGGATTC TGCGCCTAAG	1525 1530 * CCCGTGCCAA GGGCACGGTT	1535 1540 * GAGTGACGTA CTCACTGCAT	1545 1550 * AGTACCGCCT TCATGGCGGA	1555 1560 * ATAGAGTCTA TATCTCAGAT
1565 1570 * TAGGCCCACC ATCCGGGTGG	1575 1580 * CCCTTGCGTT GGGAACCGAA	1585 1590 * CTTATGCATG GAATACGTAC	1595 1600 * CTATACTGTT GATATGACAA	1605 1610 * TTTGGCTTGG AAACCGAACC	1615 1620 * GGTCTATACA CCAGATATGT
1625 1630 * CCCCCGCTTC GGGGCGGAAG	1635 1640 * CTCATGTTAT GAGTACAATA	1645 1650 * AGGTGATGGT TCCACTACCA	1655 1660 * ATAGCTTAGC TATCGAATCG	1665 1670 * CTATAGGTGT GATATCCACA	1675 1680 * GGGTTATTGA CCCAATAACT
1685 1690 * CCATTATTGA GGTAATAACT	1695 1700 * CCACTCCCCT GGTGAGGGGA	1705 1710 * ATTGGTGACG TAACCACTGC	1715 1720 * ATACTTTCCA TATGAAAGGT	1725 1730 * TTACTAATCC AATGATTAGG	1735 1740 * ATAACATGGC TATTGTACCG
1745 1750 * TCTTTGCCAC AGAAACGGTG	1755 1760 * AACTCTCTTT TTGAGAGAAA	1765 1770 * ATTGGCTATA TAACCGATAT	1775 1780 * TGCCAATACA ACGGTTATGT	1785 1790 * CTGTCCTTCA GACAGGAAGT	1795 1800 * GAGACTGACA CTCTGACTGT
1805 1810 * CGGACTCTGT GCCTGAGACA	1815 1820 * ATTTTACAG TAAAAATGTC	1825 1830 * GATGGGGTCT CTACCCCGAG	1835 1840 * CATTTATTAT GTAAATAATA	1845 1850 * TTACAAATTC AATGTTTAAG	1855 1860 * ACATATACAA TGTATATGTT
1865 1870 * CACCACCGTC GTGGTGGCAG	1875 1880 * CCCAGTGCCC GGGTCACGGG	1885 1890 * GCAGTTTTTA CGTCAAAAAT	1895 1900 * TAAACATAAA AATTTGTATT	1905 1910 * CGTGGGATCT GCACCCTAGA	1915 1920 * CCACGCGAAT GGTGCCTTA
1925 1930 * CTCGGGTACG GAGCCCATGC	1935 1940 * TGTTCCGGAC ACAAGGCTG	1945 1950 * ATGGGCTCTT TACCCGAGAA	1955 1960 * CTCCGGTAGC GAGGCCATCG	1965 1970 * GGCGGAGCTT CCGCCTCGAA	1975 1980 * CTACATCCGA GATGTAGGCT
1985 1990 * GCCCTGCTCC CGGGACGAGG	1995 2000 * CATGCCTCCA GTACGGAGGT	2005 2010 * GCGACTCATG CGCTGAGTAC	2015 2020 * GTCGCTCGGC CAGCGAGCCG	2025 2030 * AGCTCCTTGC TCGAGGAACG	2035 2040 * TCCTAACAGT AGGATTGTCA
2045 2050 * GGAGGCCAGA CCTCCGGTCT	2055 2060 * CTTAGGCACA GAATCCGTGT	2065 2070 * GCACGATGCC CGTGCTACGG	2075 2080 * CACCACCACC GTGGTGGTGG	2085 2090 * AGTGTGCCGC TCACACGGCG	2095 2100 * ACAAGGCCGT TGTTCCGGCA
2105 2110 * GGCGGTAGGG CCGCCATCCC	2115 2120 * TATGTGTCTG ATACACAGAC	2125 2130 * AAAATGAGCT TTTTACTCGA	2135 2140 * CGGGGAGCGG GCCCTCGCC	2145 2150 * GCTTGACCCG CGAACGTGGC	2155 2160 * CTGACGCATT GACTGCGTAA

FIG. 29C

2165	2170	2175	2180	2185	2190	2195	2200	2205	2210	2215	2220
	*		*		*		*		*		*
TGGAAGACTT	AAGGCAGCGG	CAGAAGAAGA	TGCAGGCAGC	TGAGTTGTTG	TGTTCTGATA	ACCTTCTGAA	TTCCGTCGCC	GTCTTCTTCT	ACGTCCGTCG	ACTCAACAAC	ACAAGACTAT
2225	2230	2235	2240	2245	2250	2255	2260	2265	2270	2275	2280
	*		*		*		*		*		*
AGAGTCAGAG	GTAAGTCCCG	TTGCGGTGCT	GTAAACGGTG	GAGGGCAGTG	TAGTCTGAGC	TCTCAGTCTC	CATTGAGGGC	AACGCCACGA	CAATTGCCAC	CTCCCGTCAC	ATCAGACTCG
2285	2290	2295	2300	2305	2310	2315	2320	2325	2330	2335	2340
	*		*		*		*		*		*
AGTACTCGTT	GCTGCCGCGC	GCGCCACCAG	ACATAATAGC	TGACAGACTA	ACAGACTGTT	TCATGAGCAA	CGACGGCGCG	CGCGGTGGTC	TGTATTATCG	ACTGTCTGAT	TGTCTGACAA
2345	2350	2355	2360	2365	2370	2375	2380	2385	2390	2395	2400
	*		*		*		*		*		*
CCTTTCCATG	GGTCTTTTCT	GCAGTCACCG	TCCTTGACAC	GAAGCTTGGG	CTGCAGGTCTG	GGAAAGGTAC	CCAGAAAAGA	CGTCAGTGGC	AGGAACTGTG	CTTCGAACCC	GACGTCCAGC
2405	2410	2415	2420	2425	2430	2435	2440	2445	2450	2455	2460
	*		*		*		*		*		*
ATCGACTCTA	GAGGATCGAT	CCCCGGGCGA	GCTCGAATTC	GCCGCCACCA	TGGAATGGAG	TAGCTGAGAT	CTCCTAGCTA	GGGGCCCGCT	CGAGCTTAAG	CGGCGGTGGT	ACCTTACCTC
2465	2470	2475	2480	2485	2490	2495	2500	2505	2510	2515	2520
	*		*		*		*		*		*
CTGGGTCTTT	CTCTTCTTCC	TGTCAGTAAC	TACAGGTGTC	CACTCCCAGG	TTCAGCTGGT	GACCCAGAAA	GAGAAGAAGG	ACAGTCATTG	ATGTCCACAG	GTGAGGGTCC	AAGTCGACCA
2525	2530	2535	2540	2545	2550	2555	2560	2565	2570	2575	2580
	*		*		*		*		*		*
TCAGTCCGGG	GCTGAGGTGA	AGAAGCCTGG	GGCCTCAGTG	AAGGTTTCTT	GTCAGGCTTC	AGTCAGGCCC	CGACTCCACT	TCTTCGGACC	CCGGAGTCAC	TTCCAAAGAA	CAGTCCGAAG
2585	2590	2595	2600	2605	2610	2615	2620	2625	2630	2635	2640
	*		*		*		*		*		*
TGGATACAGA	TTCAGTAACT	TTGTTATTCA	TTGGGTGCGC	CAGGCCCCCG	GACAGAGGTT	ACCTATGTCT	AAGTCATTGA	AACAATAAGT	AACCCACGCG	GTCCGGGGGC	CTGTCTCCAA
2645	2650	2655	2660	2665	2670	2675	2680	2685	2690	2695	2700
	*		*		*		*		*		*
TGAGTGGATG	GGATGGATCA	ATCCTTACAA	CGGAAACAAA	GAATTTTCAG	CGAAGTTCCA	ACTCACCTAC	CCTACCTAGT	TAGGAATGTT	GCCTTTGTTT	CTTAAAAGTC	GCTTCAAGGT
2705	2710	2715	2720	2725	2730	2735	2740	2745	2750	2755	2760
	*		*		*		*		*		*
GGACAGAGTC	ACCTTTACCG	CGGACACATC	CGCGAACACA	GCCTACATGG	AGTTGAGGAG	CCTGTCTCAG	TGGAAATGGC	GCCTGTGTAG	GCGCTTGTGT	CGGATGTACC	TCAACTCCTC
2765	2770	2775	2780	2785	2790	2795	2800	2805	2810	2815	2820
	*		*		*		*		*		*
CCTCAGGTCT	GCAGACACGG	CTGTTTATTA	TTGTGCGAGA	GTGGGGCCAT	ATAGTTGGGA	GGAGTCCAGA	CGTCTGTGCC	GACAAATAAT	AACACGCTCT	CACCCCGGTA	TATCAACCCT
2825	2830	2835	2840	2845	2850	2855	2860	2865	2870	2875	2880
	*		*		*		*		*		*
TGATTCTCCC	CAGGACAATT	ATTATATGGA	CGTCTGGGGC	AAAGGAACCA	CGGTCATCGT	ACTAAGAGGG	GTCCTGTAA	TAATATACCT	GCAGACCCCG	TTTCCTTGGT	GCCAGTAGCA

FIG. 29D

2885 2890	2895 2900	2905 2910	2915 2920	2925 2930	2935 2940
* *	* *	* *	* *	* *	* *
GAGCTCAGCT	TCCACCAAGG	GCCCCATCGGT	CTTCCCCCTG	GCACCCTCCT	CCAAGAGCAC
CTCGAGTCGA	AGGTGGTTCC	CGGGTAGCCA	GAAGGGGGAC	CGTGGGAGGA	GGTTCTCGTG
2945 2950	2955 2960	2965 2970	2975 2980	2985 2990	2995 3000
* *	* *	* *	* *	* *	* *
CTCTGGGGGC	ACAGCGGCCC	TGGGCTGCCT	GGTCAAGGAC	TACTTCCCCG	AACCGGTGAC
GAGACCCCCG	TGTCGCCGGG	ACCCGACGGA	CCAGTTCCTG	ATGAAGGGGC	TTGGCCACTG
3005 3010	3015 3020	3025 3030	3035 3040	3045 3050	3055 3060
* *	* *	* *	* *	* *	* *
GGTGTCGTGG	AACTCAGGCG	CCCTGACCAG	CGGCGTGCAC	ACCTTCCCCG	CTGTCTTACA
CCACAGCACC	TTGAGTCCGC	GGGACTGGTC	GCCGCACGTG	TGGAAGGGCC	GACAGGATGT
3065 3070	3075 3080	3085 3090	3095 3100	3105 3110	3115 3120
* *	* *	* *	* *	* *	* *
GTCCTCAGGA	CTCTACTCCC	TCAGCAGCGT	GGTGACCGTG	CCCTCCAGCA	GCTTGGGCAC
CAGGAGTCCT	GAGATGAGGG	AGTCGTGCGA	CCACTGGCAC	GGGAGGTCTG	CGAACCCGTG
3125 3130	3135 3140	3145 3150	3155 3160	3165 3170	3175 3180
* *	* *	* *	* *	* *	* *
CCAGACCTAC	ATCTGCAACG	TGAATCACAA	GCCCAGCAAC	ACCAAGGTGG	ACAAGAAAGT
GGTCTGGATG	TAGACGTTGC	ACTTAGTGTT	CGGGTCGTTG	TGGTTCACAC	TGTTCTTTCA
3185 3190	3195 3200	3205 3210	3215 3220	3225 3230	3235 3240
* *	* *	* *	* *	* *	* *
TGGTGAGAGG	CCAGCACAGG	GAGGGAGGGT	GTCTGCTGGA	AGCCAGGCTC	AGCGCTCCTG
ACCACTCTCC	GGTCGTGTCC	CTCCCTCCCA	CAGACGACCT	TCGGTCCGAG	TCGCGAGGAC
3245 3250	3255 3260	3265 3270	3275 3280	3285 3290	3295 3300
* *	* *	* *	* *	* *	* *
CCTGGACGCA	TCCCCGGCTAT	GCAGCCCCAG	TCCAGGGCAG	CAAGGCAGGC	CCCGTCTGCC
GGACCTGCGT	AGGGCCGATA	CGTCGGGGTC	AGGTCCCGTC	GTTCCGTCCG	GGGCAGACGG
3305 3310	3315 3320	3325 3330	3335 3340	3345 3350	3355 3360
* *	* *	* *	* *	* *	* *
TCTTACCCCG	GAGGCCCTCTG	CCCGCCCCAC	TCATGCTCAG	GGAGAGGGTC	TTCTGGCTTT
AGAAGTGGGC	CTCCGGAGAC	GGGCGGGGTG	AGTACGAGTC	CCTCTCCAG	AAGACCGAAA
3365 3370	3375 3380	3385 3390	3395 3400	3405 3410	3415 3420
* *	* *	* *	* *	* *	* *
TTCCCCAGGC	TCTGGGCAGG	CACAGGCTAG	GTGCCCCATA	CCCAGGCCCT	GCACACAAAG
AAGGGGTCCG	AGACCCGTCC	GTGTCCGATC	CACGGGGATT	GGGTCCGGGA	CGTGTGTTTC
3425 3430	3435 3440	3445 3450	3455 3460	3465 3470	3475 3480
* *	* *	* *	* *	* *	* *
GGGCAGGTGC	TGGGCTCAGA	CCTGCCAAGA	GCCATATCCG	GGAGGACCCT	GCCCCTGACC
CCCGTCCACG	ACCCGAGTCT	GGACGGTTCT	CGGTATAGGC	CCTCCTGGGA	CGGGGACTGG
3485 3490	3495 3500	3505 3510	3515 3520	3525 3530	3535 3540
* *	* *	* *	* *	* *	* *
TAAGCCCACC	CCAAAGGCCA	AACTCTCCAC	TCCCTCAGCT	CGGACACCTT	CTCTCCTCCC
ATTGCGGTGG	GGTTTCCGGT	TTGAGAGGTG	AGGGAGTCGA	GCCTGTGGAA	GAGAGGAGGG
3545 3550	3555 3560	3565 3570	3575 3580	3585 3590	3595 3600
* *	* *	* *	* *	* *	* *
AGATTTCGAGT	AACTCCCAAT	CTTCTCTCTG	CAGAGCCCAA	ATCTTGTGAC	AAAACTCACA
TCTAAGCTCA	TTGAGGGTTA	GAAGAGAGAC	GTCTCGGGTT	TAGAACACTG	TTTTGAGTGT

FIG. 29E

3605 3610 *	3615 3620 *	3625 3630 *	3635 3640 *	3645 3650 *	3655 3660 *
CATGCCCACC GTACGGGTGG	GTGCCCAGGT CACGGGTCCA	AAGCCAGCCC TTCGGTCGGG	AGGCCTCGCC TCCGGAGCGG	CTCCAGCTCA GAGGTCGAGT	AGGCGGGACA TCCGCCCTGT
3665 3670 *	3675 3680 *	3685 3690 *	3695 3700 *	3705 3710 *	3715 3720 *
GGTGCCCTAG CCACGGGATC	AGTAGCCTGC TCATCGGACG	ATCCAGGGAC TAGGTCCTTG	AGGCCCCAGC TCCGGGGTCG	CGGGTGCTGA GCCCACGACT	CACGTCCACC GTGCAGGTGG
3725 3730 *	3735 3740 *	3745 3750 *	3755 3760 *	3765 3770 *	3775 3780 *
TCCATCTCTC AGGTAGAGAG	CCTCAGCACC GGAGTCGTGG	TGAGGCCGCG ACTCCGGCGC	GGAGGACCAT CCTCCTGGTA	CAGTCTTCCT GTCAGAAGGA	CTTCCCCCCA GAAGGGGGGT
3785 3790 *	3795 3800 *	3805 3810 *	3815 3820 *	3825 3830 *	3835 3840 *
AAACCCAAGG TTTGGGTTCC	ACACCCTCAT TGTGGGAGTA	GATCTCCCGG CTAGAGGGCC	ACCCCTGAGG TGGGGACTCC	TCACATGCGT AGTGACGCA	GGTGGTGGAC CCACCACCTG
3845 3850 *	3855 3860 *	3865 3870 *	3875 3880 *	3885 3890 *	3895 3900 *
GTGAGCCACG CACTCGGTGC	AAGACCCTGA TTCTGGGACT	GGTCAAGTTC CCAGTTCAAG	AACTGGTACG TTGACCATGC	TGGACGGCGT ACCTGCCGCA	GGAGGTGCAT CCTCCACGTA
3905 3910 *	3915 3920 *	3925 3930 *	3935 3940 *	3945 3950 *	3955 3960 *
AATGCCAAGA TTACGGTTCT	CAAAGCCGCG GTTTCGGCGC	GGAGGAGCAG CCTCCTCGTC	TACAACAGCA ATGTTGTCGT	CGTACCGTGT GCATGGCACA	GGTCAGCGTC CCAGTCGCAG
3965 3970 *	3975 3980 *	3985 3990 *	3995 4000 *	4005 4010 *	4015 4020 *
CTCACCGTCC GAGTGGCAGG	TGCACCAGGA ACGTGGTCCT	CTGGCTGAAT GACCGACTTA	GGCAAGGAGT CCGTTCTCTA	ACAAGTGCAA TGTTACGTT	GGTCTCCAAC CCAGAGGTTG
4025 4030 *	4035 4040 *	4045 4050 *	4055 4060 *	4065 4070 *	4075 4080 *
AAAGCCCTCC TTTCGGGAGG	CAGCCCCCAT GTCGGGGGTA	CGAGAAAACC GCTCTTTTGG	ATCTCCAAAG TAGAGGTTTC	CCAAAGGTGG GGTTTCCACC	GACCCGTGGG CTGGGCACCC
4085 4090 *	4095 4100 *	4105 4110 *	4115 4120 *	4125 4130 *	4135 4140 *
GTGCGAGGGC CACGCTCCCC	CACATGGACA GTGTACCTGT	GAGGCCGGCT CTCCGGCCGA	CGGCCCACCC GCGGGGTGGG	TCTGCCCTGA AGACGGGACT	GAGTGACCGC CTCACTGGCG
4145 4150 *	4155 4160 *	4165 4170 *	4175 4180 *	4185 4190 *	4195 4200 *
TGTACCAACC ACATGGTTGG	TCTGTCCCTA AGACAGGGAT	CAGGGCAGCC GTCCCGTCGG	CCGAGAACCA GGCTCTTGCT	CAGGTGTACA GTCCACATGT	CCCTGCCCCC GGGACGGGGG
4205 4210 *	4215 4220 *	4225 4230 *	4235 4240 *	4245 4250 *	4255 4260 *
ATCCCGGGAT TAGGGCCCTA	GAGCTGACCA CTCGACTGGT	AGAACCAGGT TCTTGGTCCA	CAGCCTGACC GTCCGACTGG	TGCCTGGTCA ACGGACCAGT	AAGGCTTCTA TTCCGAAGAT
4265 4270 *	4275 4280 *	4285 4290 *	4295 4300 *	4305 4310 *	4315 4320 *
TCCCAGCGAC AGGGTCGCTG	ATCGCCGTGG TAGCGGCACC	AGTGGGAGAG TCACCCTCTC	CAATGGGCAG GTTACCCGTC	CCGAGAAACA GGCCTCTTGT	ACTACAAGAC TGATGTTCTG

FIG. 29F

4325 4330	4335 4340	4345 4350	4355 4360	4365 4370	4375 4380
* *	* *	* *	* *	* *	* *
CACGCCTCCC	GTGCTGGA	CCGACGGCTC	CTTCTTCCTC	TACAGCAAGC	TCACCGTGGA
GTGCGGAGGG	CACGACCTGA	GGCTGCCGAG	GAAGAAGGAG	ATGTCGTTCC	ACTGGCACCT
4385 4390	4395 4400	4405 4410	4415 5520	4425 4430	4435 4440
* *	* *	* *	* *	* *	* *
CAAGAGCAGG	TGGCAGCAGG	GGAACGTCTT	CTCATGCTCC	GTGATGCATG	AGGCTCTGCA
GTTCTCGTCC	ACCGTCGTCC	CCTTGCAGAA	GAGTACGAGG	CACTACGTAC	TCCGAGACGT
4445 4450	4455 4460	4465 4470	4475 4480	4485 4490	4495 4500
* *	* *	* *	* *	* *	* *
CAACCACTAC	ACGCAGAAGA	GCCTCTCCCT	GTCTCCGGGT	AAATGAGTGC	GACGGCCGGC
GTTGGTGATG	TGCGTCTTCT	CGGAGAGGGA	CAGAGGCCCA	TTTACTCAGC	CTGCCGGGCC
4505 4510	4515 4520	4525 4530	4535 4540	4545 4550	4555 4560
* *	* *	* *	* *	* *	* *
AAGCCCCCGC	TCCCCGGGCT	CTCGCGGTCC	CACGAGGATG	CTTGGCACGT	ACCCCTGTGA
TTCGGGGGCG	AGGGGCCCCA	GAGCGCCAGC	GTGCTCCTAC	GAACCGTGCA	TGGGGGACAT
4565 4570	4575 4580	4585 4590	4595 4600	4605 4610	4615 4620
* *	* *	* *	* *	* *	* *
CATACTTCCC	GGGCGCCCAG	CATGGAAATA	AAGCACCCAG	CGCTGCCCTG	GGCCCTGCG
GTATGAAGGG	CCCGCGGGTC	GTACCTTTAT	TTCGTGGGTC	GCGACGGGAC	CCGGGGACGC
4625 4630	4635 4640	4645 4650	4655 4660	4665 4670	4675 4680
* *	* *	* *	* *	* *	* *
AGACTGTGAT	GGTTCTTTCC	ACGGGTCAGG	CCGAGTCTGA	GGCCTGAGTG	GCATGAGGGA
TCTGACACTA	CCAAGAAAGG	TGCCCAGTCC	GGCTCAGACT	CCGGACTCAC	CGTACTCCCT
4685 4690	4695 4700	4705 4710	4715 4720	4725 4730	4735 4740
* *	* *	* *	* *	* *	* *
GGCAGAGCGG	GTCCCACTGT	CCCCACACTG	GCCCAGGCTG	TGCAGGTGTG	CCTGGGCGCG
CCGTCTCGCC	CAGGGTGACA	GGGGTGTGAC	CGGGTCCGAC	ACGTCCACAC	GGACCCGGCG
4745 4750	4755 4760	4765 4770	4775 4780	4785 4790	4795 4800
* *	* *	* *	* *	* *	* *
CTAGGGTGGG	GCTCAGCCAG	GGGCTGCCCT	CGGCAGGGTG	GGGGATTTCG	CAGCGTTGCC
GATCCCAACC	CGAGTCGGTC	CCCGACGGGA	GCCGTCCAC	CCCCTAAACG	GTCGCAACGG
4805 4810	4815 5820	4825 4830	4835 4840	4845 4850	4855 4860
* *	* *	* *	* *	* *	* *
CTCCCTCCAG	CAGCACCTGC	CCTGGGCTGG	GCCACGGGAA	GCCCTAGGAG	CCCCTGGGGA
GAGGGAGGTC	GTCGTGGACG	GGACCCGACC	CGGTGCCCTT	CGGGATCCTC	GGGGACCCCT
4865 4870	4875 4880	4885 4890	4895 4900	4905 4910	4915 4920
* *	* *	* *	* *	* *	* *
CAGACACACA	GCCCCTGCCT	CTGTAGGAGA	CTGTCCTGTT	CTGTGAGCGC	CCTGTCCTCC
GTCTGTGTGT	CGGGGACGGA	GACATCCTCT	GACAGGACAA	GACACTCGCG	GGACAGGAGG
4925 4930	4935 4940	4945 4950	4955 4960	4965 4970	4975 4980
* *	* *	* *	* *	* *	* *
GACCTCCATG	CCCACTCGGG	GGCATGCCTA	GTCCATGTGC	GTAGGGACAG	GCCCTCCCTC
CTGGAGGTAC	GGGTGAGCCC	CCGTACGGAT	CAGGTACACG	CATCCCTGTC	CGGGAGGGAG
4985 4990	4995 5000	5005 5010	5015 5020	5025 5030	5035 5040
* *	* *	* *	* *	* *	* *
ACCCATCTAC	CCCCACGGCA	CTAACCCCTG	GCTGTCCTGC	CCAGCCTCGC	ACCCGCATGG
TGGGTAGATG	GGGGTGCCGT	GATTGGGGAC	CGACAGGACG	GGTCGGAGCG	TGGGCGTACC

FIG. 29G

5045 5050	5055 5060	5065 5070	5075 5080	5085 5090	5095 5100
* *	* *	* *	* *	* *	* *
GGACACAACC	GA CTCCGGGG	ACATGCACTC	TCGGGGCCCTG	TGGAGGGACT	GGTGCAGATG
CCTGTGTTGG	CTGAGGCCCC	TGTACGTGAG	AGCCCCGGGAC	ACCTCCCTGA	CCACGTCTAC
5105 5110	5115 5120	5125 5130	5135 5140	5145 5150	5155 5160
* *	* *	* *	* *	* *	* *
CCCACACACA	CACTCAGTCC	AGACCCGTTC	AACAAAACCC	CCGCACTGAG	GTTGGCCGGC
GGGTGTGTGT	GTGAGTCAGG	TCTGGGCAAG	TTGTTTTGGG	GGCGTGACTC	CAACCGGCCG
5165 5170	5175 5180	5185 5190	5195 5200	5205 5210	5215 5220
* *	* *	* *	* *	* *	* *
CACACGGCCA	CCACACACAC	ACGTGCACGC	CTCACACACG	GAGCCTCACC	CGGGCGAACT
GTGTGCCGGT	GGTGTGTGTG	TGCACGTGCG	GAGTGTGTGC	CTCGGAGTGG	GCCCCGCTTGA
5225 5230	5235 5240	5245 5250	5255 5260	5265 5270	5275 5280
* *	* *	* *	* *	* *	* *
GCACAGCACC	CAGACCAGAG	CAAGGTCTCT	GCACACGTGA	ACACTCCTCG	GACACAGGCC
CGTGTCTGTT	GTCTGGTCTC	GTTCCAGGAG	CGTGTGCACT	TGTGAGGAGC	CTGTGTCCGG
5285 5290	5295 5300	5305 5310	5315 5320	5325 5330	5335 5340
* *	* *	* *	* *	* *	* *
CCCACGAGCC	CCACGCGGCA	CCTCAAGGCC	CACGAGCCTC	TCGGCAGCTT	CTCCACATGC
GGGTGCTCGG	GGTGCGCCGT	GGAGTTCGGG	GTGCTCGGAG	AGCCGTCGAA	GAGGTGTACG
5345 5350	5355 5360	5365 5370	5375 5380	5385 5390	5395 5400
* *	* *	* *	* *	* *	* *
TGACCTGCTC	AGACAAAACCC	AGCCCTCCTC	TCACAAGGGT	GCCCCTGCAG	CCGCCACACA
ACTGGACGAG	TCTGTTTGGG	TCGGGAGGAG	AGTGTTCCCA	CGGGGACGTC	GGCGGTGTGT
5405 5410	5415 5420	5425 5430	5435 5440	5445 5450	5455 5460
* *	* *	* *	* *	* *	* *
CACACAGGGG	ATCACACACC	ACGTACAGTC	CCTGGCCCTG	GCCCCACTTC	CAGTGCCGCC
GTGTGTCCCC	TAGTGTGTGG	TGCAGTGCAG	GGACCGGGAC	CGGGTGAAGG	GTCACGGCGG
5465 5470	5475 5480	5485 5490	5495 5500	5505 5510	5515 5520
* *	* *	* *	* *	* *	* *
CTTCCCTGCA	GGGCGGATCA	TAATCAGCCA	TACCACATTT	GTAGAGGTTT	TACTTGCTTT
GAAGGGACGT	CCCGCCTAGT	ATTAGTCGGT	ATGGTGTAAG	CATCTCCAAA	ATGAACGAAA
5525 5530	5535 5540	5545 5550	5555 5560	5565 5570	5575 5580
* *	* *	* *	* *	* *	* *
AAAAAACCTC	CCACACCTCC	CCCTGAACCT	GAAACATAAA	ATGAATGCAA	TTGTTGTTGT
TTTTTTGGAG	GGTGTGGAGG	GGGACTTGGA	CTTTGTATTT	TACTTACGTT	AACAACAACA
5585 5590	5595 5600	5605 5610	5615 5620	5625 5630	5635 5640
* *	* *	* *	* *	* *	* *
TAACTTGTTT	ATTGCAGCTT	ATAATGGTTA	CAAATAAAGC	AATAGCATCA	CAAATTTTAC
ATTGAACAAA	TAACGTCGAA	TATTACCAAT	GTTTATTTTC	TTATCGTAGT	GTTTAAAGTG
5645 5650	5655 5660	5665 5670	5675 5680	5685 5690	5695 5700
* *	* *	* *	* *	* *	* *
AAATAAAGCA	TTTTTTTTCAC	TGCATTCTAG	TTGTGGTTTG	TCCAAACTCA	TCAATGTATC
TTTATTTTCGT	AAAAAAAAGTG	ACGTAAGATC	AACACCAAAC	AGGTTTGAGT	AGTTACATAG
5750 5710	5715 5720	5725 5730	5735 5740	5745 5750	5755 5760
* *	* *	* *	* *	* *	* *
TTATCATGTC	TGAGATCCTC	TACGCCGGAC	GCATCGTGGC	CGGCATCACC	GGCGCCACAG
AATAGTACAG	ACTCTAGGAG	ATGCGGCCTG	CGTAGCACCG	GCCGTAGTGG	CCGCGGTGTC

FIG. 29H

5765	5770	5775	5780	5785	5790	5795	5800	5805	5810	5815	5820
	*		*		*		*		*		*
GTGCGGTTGC	TGGCGCCTAT	ATCGCCGACA	TCACCGATGG	GGAAGATCGG	GCTCGCCACT						
CACGCCAACG	ACCGCGGATA	TAGCGGCTGT	AGTGGCTACC	CCTTCTAGCC	CGAGCGGTGA						
5825	5830	5835	5840	5845	5850	5855	5860	5865	5870	5875	5880
	*		*		*		*		*		*
TCGGGCTCAT	GAGCGCTTGT	TTCGGCGTGG	GTATGGTGGC	AGGCCCCGTGG	CCGGGGGACT						
AGCCCCGAGTA	CTCGCGAACA	AAGCCGCACC	CATACCACCG	TCCGGGCACC	GGCCCCCTGA						
5885	5890	5895	5900	5905	5910	5915	5920	5925	5930	5935	5940
	*		*		*		*		*		*
GTTGGGCGCC	ATCTCCTTGC	ATGCACCATT	CCTTGCGGCG	GCGGTGCTCA	ACGGCCTCAA						
CAACCCGCGG	TAGAGGAACG	TACGTGGTAA	GGAACGCCGC	CGCCACGAGT	TGCCGGAGTT						
5945	5950	5955	5960	5965	5970	5975	5980	5985	5990	5990	6000
	*		*		*		*		*		*
CCTACTACTG	GGCTGCTTCC	TAATGCAGGA	GTCGCATAAG	GGAGAGCGTC	GACCTCGGGC						
GGATGATGAC	CCGACGAAGG	ATTACGTCCT	CAGCGTATTC	CCTCTCGCAG	CTGGAGCCCC						
6005	6010	6015	6020	6025	6030	6035	6040	6045	6050	6055	6060
	*		*		*		*		*		*
CGCGTTGCTG	GCGTTTTTCC	ATAGGCTCCG	CCCCCCTGAC	GAGCATCACA	AAAATCGACG						
GCGCAACGAC	CGCAAAAAGG	TATCCGAGGC	GGGGGGACTG	CTCGTAGTGT	TTTTAGCTGC						
6065	6070	6075	6080	6085	6090	6095	6100	6105	6110	6115	6120
	*		*		*		*		*		*
CTCAAGTCAG	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	TACCAGGCGT	TTCCCCCTGG						
GAGTTCAGTC	TCCACCGCTT	TGGGCTGTCC	TGATATTTCT	ATGGTCCGCA	AAGGGGGACC						
6125	6130	6135	6140	6145	6150	6155	6160	6165	6170	6175	6180
	*		*		*		*		*		*
AAGCTCCCTC	GTGCGCTCTC	CTGTTCCGAC	CCTGCCGCTT	ACCGGATACC	TGTCCGCCTT						
TTTCAGGGAG	CACGCGAGAG	GACAAGGCTG	GGACGGCGAA	TGGCCTATGG	ACAGGCGGAA						
6185	6190	6195	6200	6205	6210	6215	6220	6225	6230	6235	6240
	*		*		*		*		*		*
TCTCCCTTCG	GGAAGCGTGG	CGCTTCTCTCA	ATGCTCACGC	TGTAGGTATC	TCAGTTCGGT						
AGAGGGAAGC	CCTTCGCACC	GCGAAAGAGT	TACGAGTGCG	ACATCCATAG	AGTCAAGCCA						
6245	6250	6255	6260	6265	6270	6275	6280	6285	6290	6295	6300
	*		*		*		*		*		*
GTAGGTCGTT	CGCTCCAAGC	TGGGCTGTGT	GCACGAACCC	CCCGTTCAGC	CCGACCGCTG						
CATCCAGCAA	GCGAGGTTCTG	ACCCGACACA	CGTGCTTGGG	GGGCAAGTCG	GGCTGGCGAC						
6305	6310	6315	6320	6325	6330	6335	6340	6345	6350	6355	6360
	*		*		*		*		*		*
CGCCTTATCC	GGTAACTATC	GTCTTGAGTC	CAACCCGGTA	AGACACGACT	TATCGCCACT						
GCGGAATAGG	CCATTGATAG	CAGAACTCAG	GTTGGGCCAT	TCTGTGCTGA	ATAGCGGTGA						
6365	6370	6375	6380	6385	6390	6395	6400	6405	6410	6415	6420
	*		*		*		*		*		*
GGCAGCAGCC	ACTGGTAACA	GGATTAGCAG	AGCGAGGTAT	GTAGGCGGTG	CTACAGAGTT						
CCGTGCTCGG	TGACCATTGT	CCTAATCGTC	TCGCTCCATA	CATCCGCCAC	GATGTCTCAA						
6425	6430	6435	6440	6445	6450	6455	6460	6465	6470	6475	6480
	*		*		*		*		*		*
CTTGAAGTGG	TGGCCTAACT	ACGGCTACAC	TAGAAGGACA	GTATTTGGTA	TCTGCGCTCT						
GAACTTCACC	ACCGGATTGA	TGCCGATGTG	ATCTTCCTGT	CATAAACCAT	AGACGCGAGA						

FIG. 291

6485 6490	6495 6500	6505 6510	6515 6520	6525 6530	6535 6540
* *	* *	* *	* *	* *	* *
GCTGAAGCCA	GTTACCTTCG	GAAAAAGAGT	TGGTAGCTCT	TGATCCGGCA	AACAAACCAC
CGACTTCGGT	CAATGGAAGC	CTTTTCTCA	ACCATCGAGA	ACTAGGCCGT	TTGTTTGGTG
6545 6550	6555 6560	6565 6570	6575 6580	6585 6590	6595 6600
* *	* *	* *	* *	* *	* *
CGCTGGTAGC	GGTGGTTTTT	TTGTTTGCAA	GCAGCAGATT	ACGCGCAGAA	AAAAAGGATC
GCGACCATCG	CCACCAAAAA	AACAAACGTT	CGTCGTCTAA	TGCGCGTCTT	TTTTTCCTAG
6605 6610	6615 6620	6625 6630	6635 6640	6645 6650	6655 6660
* *	* *	* *	* *	* *	* *
TCAAGAAGAT	CCTTTGATCT	TTTCTACGGG	GTCTGACGCT	CAGTGGAAACG	AAAACCTCAG
AGTTCTTCTA	GGAAACTAGA	AAAGATGCCC	CAGACTGCGA	GTCACCTTGC	TTTTGAGTGC
6665 6670	6675 6680	6685 6690	6695 6700	6705 6710	6715 6720
* *	* *	* *	* *	* *	* *
TTAAGGGATT	TTGGTCATGA	GATTATCAAA	AAGGATCTTC	ACCTAGATCC	TTTTAAATTA
AATTCCCTAA	AACCAGTACT	CTAATAGTTT	TTCTAGTAAG	TGGATCTAGG	AAAATTTAAT
6725 6730	6735 6740	6745 6750	6755 6760	6765 6770	6775 6780
* *	* *	* *	* *	* *	* *
AAAATGAAGT	TTTAAATCAA	TCTAAAGTAT	ATATGAGTAA	ACTTGGTCTG	ACAGTTACCA
TTTTACTTCA	AAATTTAGTT	AGATTTCATA	TATACTCATT	TGAACCAGAC	TGTCAATGGT
6785 6790	6795 6800	6805 6810	6815 6820	6825 6830	6835 6840
* *	* *	* *	* *	* *	* *
ATGCTTAATC	AGTGAGGCAC	CTATCTCAGC	GATCTGTCTA	TTTCGTTTCAT	CCATAGTTGC
TACGAATTAG	TCACTCCGTG	GATAGAGTCG	CTAGACAGAT	AAAGCAAGTA	GGTATCAACG
6845 6850	6855 6860	6865 6870	6875 6880	6885 6890	6895 6900
* *	* *	* *	* *	* *	* *
CTGACTCCCC	GTCGTGTAGA	TAACTACGAT	ACGGGAGGGC	TTACCATCTG	GCCCCAGTGC
GACTGAGGGG	CAGCACATCT	ATTGATGCTA	TGCCCTCCCG	AATGGTAGAC	CGGGGTACAG
6905 6910	6915 6920	6925 6930	6935 6940	6945 6950	6955 6960
* *	* *	* *	* *	* *	* *
TGCAATGATA	CCGCGAGACC	CACGCTCACC	GGCTCCAGAT	TTATCAGCAA	TAAACCAGCC
ACGTTACTAT	GGCGCTCTGG	GTGCGAGTGG	CCGAGGTCTA	AATAGTCGTT	ATTTGGTCGG
6965 6970	6975 6980	6985 6990	6995 7000	7005 7010	7015 7020
* *	* *	* *	* *	* *	* *
AGCCGGAAGG	GCCGAGCGCA	GAAGTGGTCC	TGCAACTTTA	TCCGCCTCCA	TCCAGTCTAT
TCGGCCTTCC	CGGCTCGCGT	CTTCACCAGG	ACGTTGAAAT	AGGCGGAGGT	AGGTCAGATA
7025 7030	7035 7040	7045 7050	7055 7060	7065 7070	7075 7080
* *	* *	* *	* *	* *	* *
TAATTGTTGC	CGGGAAGCTA	GAGTAAGTAG	TTCGCCAGTT	AATAGTTTGC	GCAACGTTGT
ATTAACAACG	GCCCTTCGAT	CTCATTCATC	AAGCGGTCAA	TTATCAAACG	CGTTGCAACA
7085 7090	7095 7100	7105 7110	7115 7120	7125 7130	7135 7140
* *	* *	* *	* *	* *	* *
TGCCATTGCT	ACAGGCATCG	TGGTGTACAG	CTCGTCGTTT	GGTATGGCTT	CATTACAGCTC
ACGGTAACGA	TGTCCGTAGC	ACCACAGTGC	GAGCAGCAAA	CCATACCGAA	GTAAGTCGAG
7145 7150	7155 7160	7165 7170	7175 7180	7185 7190	7195 7200
* *	* *	* *	* *	* *	* *
CGGTTCCCAA	CGATCAAGGC	GAGTTACATG	ATCCCCCATG	TTGTGCAAAA	AAGCGGTTAG
GCCAAGGGTT	GCTAGTTCCG	CTCAATGTAC	TAGGGGGTAC	AACACGTTTT	TTCGCCAATC

FIG. 29J

7205 7210 * CTCCTTCGGT GAGGAAGCCA	7215 7220 * CCTCCGATCG GGAGGCTAGC	7225 7230 * TTGTCAGAAG AACAGTCTTC	7235 7240 * TAAGTTGGCC ATTCAACCGG	7245 7250 * GCAGTGTTAT CGTCACAATA	7255 7260 * CACTCATGGT GTGAGTACCA
7265 7270 * TATGGCAGCA ATACCGTCGT	7275 7280 * CTGCATAATT GACGTATTAA	7285 7290 * CTCTTACTGT GAGAATGACA	7295 7300 * CATGCCATCC GTACGGTAGG	7305 7310 * GTAAGATGCT CATTCTACGA	7315 7320 * TTTCTGTGAC AAAGACACTG
7325 7330 * TGGTGAGTAC ACCACTCATG	7335 7340 * TCAACCAAGT AGTTGGTTCA	7345 7350 * CATTCTGAGA GTAAGACTCT	7355 7360 * ATAGTGATG TATCACATAC	7365 7370 * CGGCGACCGA GCCGCTGGCT	7375 7380 * GTTGCTCTTG CAACGAGAAC
7385 7390 * CCCGGCGTCA GGGCGCAGT	7395 7400 * ACACGGGATA TGTGCCCTAT	7405 7410 * ATACCGCGCC TATGGCGCGG	7415 7420 * ACATAGCAGA TGTATCGTCT	7425 7430 * ACTTTAAAAG TGAAATTTTC	7435 7440 * TGCTCATCAT ACGAGTAGTA
7445 7450 * TGAAAAACGT ACCTTTTGCA	7455 7460 * TCTTCGGGGC AGAAGCCCCG	7465 7470 * GAAAACTCTC CTTTTGAGAG	7475 7480 * AAGGATCTTA TTCCTAGAAT	7485 7490 * CCGCTGTTGA GGCGACAAC	7495 7500 * GATCCAGTTC CTAGGTCAAG
7505 7510 * GATGTAACCC CTACATTGGG	7515 7520 * ACTCGTGCAC TGAGCACGTG	7525 7530 * CCAACTGATC GGTTGACTAG	7535 7540 * TTCAGCATCT AAGTCGTAGA	7545 7550 * TTTACTTTCA AAATGAAAGT	7555 7560 * CCAGCGTTTC GGTCGCAAG
7565 7570 * TGGGTGAGCA ACCCACTCGT	7575 7580 * AAAACAGGAA TTTTGTCCTT	7585 7590 * GGCAAAATGC CCGTTTTTACG	7595 7600 * CGCAAAAAAG GCGTTTTTTC	7605 7610 * GGAATAAGGG CCTTATTCCC	7615 7620 * CGACACGGAA GCTGTGCCTT
7625 7630 * ATGTTGAATA TACAACTTAT	7635 7640 * CTCATACTCT GAGTATGAGA	7645 7650 * TCCTTTTTTCA AGGAAAAAGT	7655 7660 * ATATTATTGA TATAATAACT	7665 7670 * AGCATTATATC TCGTAAATAG	7675 7680 * AGGGTTATTG TCCCAATAAC
7685 7690 * TCTCATGAGC AGAGTACTCG	7695 7700 * GGATACATAT CCTATGTATA	7705 7710 * TTGAATGTAT AACTTACATA	7715 7720 * TTAGAAAAAT AATCTTTTTA	7725 7730 * AAACAAATAG TTTGTTTATC	7735 7740 * GGGTTCCGCG CCCAAGGCGC
7745 7750 * CACATTTCCC GTGTAAAGGG	7755 7760 * CGAAAAAGTGC GCTTTTTCACG	7765 7770 * CACCTGACGT GTGGACTGCA	7775 7780 * CTAAGAAACC GATTCTTTGG	7785 7790 * ATTATTATCA TAATAATAGT	7795 7800 * TGACATTAAC ACTGTAATTG
7805 7810 * CTATAAAAAAT GATATTTTTTA	7815 7820 * AGGCGTATCA TCCGCATAGT	7825 7830 * CGAGGCCCTG GCTCCGGGAC	7835 7840 * ATGGCTCTTT TACCGAGAAA	7845 7850 * GCGGCACCCA CGCCGTGGGT	7855 7860 * TCGTTTCGTAA AGCAAGCATT
7865 7870 * TGTTCCGTGG ACAAGGCACC	7875 7880 * CACCGAGGAC GTGGCTCCTG	7885 7890 * AACCCTCAAG TTGGGAGTTC	7895 7900 * AGAAAAATGTA TCTTTTACAT	7905 7910 * ATCACACTGG TAGTGTGACC	7915 7920 * CTCACCTTGG GAGTGGAAGC

FIG. 29K

7925 7930	7935 7940	7945 7950	7955 7960	7965 7970	7975 7980
* *	* *	* *	* *	* *	* *
GGTGGGCCTT	TCTGCGTTTA	TAAGGAGACA	CTTTATGTTT	AAGAAGGTTG	GTAAATTCCT
CCACCCGGA	AGACGCAAAT	ATTCCTCTGT	GAAATACAAA	TTCTTCCAAC	CATTTAAGGA
7985 7990	7995 8000	8005 8010	8015 8020	8025 8030	8035 8040
* *	* *	* *	* *	* *	* *
TGCGGCTTTG	GCAGCCAAGC	TAGATCCGGC	TGTGGAATGT	GTGTCAGTTA	GGGTGTGGAA
ACGCCGAAAC	CGTCGGTTCG	ATCTAGGCCG	ACACCTTACA	CACAGTCAAT	CCCACACCTT
8045 8050	8055 8060	8065 8070	8075 8080	8085 8090	8095 8100
* *	* *	* *	* *	* *	* *
AGTCCCCAGG	CTCCCCAGCA	GGCAGAAAGTA	TGCAAAGCAT	GCATCTCAAT	TAGTCAGCAA
TCAGGGGTCC	GAGGGGTCTG	CCGTCTTCAT	ACGTTTCGTA	CGTAGAGTTA	ATCAGTCGTT
8105 8110	8115 8120	8125 8130	8135 8140	8145 8150	8155 8160
* *	* *	* *	* *	* *	* *
CCAGGCTCCC	CAGCAGGCAG	AAGTATGCAA	AGCATGCATC	TCAATTAGTC	AGCAACCATA
GGTCCGAGGG	GTCGTCCGTC	TTCATACGTT	TGCTACGTAG	AGTTAATCAG	TCGTTGGTAT
8165 8170	8175 8180	8185 8190	8195 8200	8205 8210	8215 8220
* *	* *	* *	* *	* *	* *
GTCCCGCCCC	TAAGTCCGCC	CATCCCGCCC	CTAACTCCGC	CCAGTTCCGC	CCATTCTCCG
CAGGGCGGGG	ATTGAGGCGG	GTAGGGCGGG	GATTGAGGCG	GGTCAAGGCG	GGTAAGAGGC
8225 8230	8235 8240	8245 8250	8255 8260	8265 8270	8275 8280
* *	* *	* *	* *	* *	* *
CCCCATGGCT	GACTAATTTT	TTTTATTTAT	GCAGAGGCCG	AGGCCGCCTC	GGCCTCTGAG
GGGGTACCGA	CTGATTAAAA	AAAATAAATA	CGTCTCCGGC	TCCGGCGGAG	CCGGAGACTC
8285 8290	8295 8300	8305 8310	8315 8320	8325 8330	8335 8340
* *	* *	* *	* *	* *	* *
CTATTCCAGA	AGTAGTGAGG	AGGCTTTTTT	GGAGGCCTAG	GCTTTTGCAA	AAACTAGCTT
GATAAGGTCT	TCATCACTCC	TCCGAAAAAA	CCTCCGGATC	CGAAAACGTT	TTTGATCGAA
8345 8350	8355 8360	8365 8370	8375 8380	8385 8390	8395 8400
* *	* *	* *	* *	* *	* *
GGGGCCACCG	CTCAGAGCAC	CTTCCACCAT	GGCCACCTCA	GCAAGTTCCC	ACTTGAACAA
CCCCGGTGGC	GAGTCTCGTG	GAAGGTGGTA	CCGGTGGAGT	CGTTCAAGGG	TGAACTTGTT
8405 8410	8415 8420	8425 8430	8435 8440	8445 8550	8455 8460
* *	* *	* *	* *	* *	* *
AAACATCAAG	CAAATGTACT	TGTGCCTGCC	CCAGGGTGAG	AAAGTCCAAG	CCATGTATAT
TTTGTAGTTC	GTTTACATGA	ACACGGACGG	GGTCCCACTC	TTTCAGGTTC	GGTACATATA
8465 8470	8475 8480	8485 8490	8495 8500	8505 8510	8515 8520
* *	* *	* *	* *	* *	* *
CTGGGTTGAT	GGTACTGGAG	AAGGACTCCG	CTGCAAAACC	CGCACCTCTG	ACTGTGAGCC
GACCCAACTA	CCATGACCTC	TTCCTGACGC	GACGTTTTTG	GCGTGGGACC	TGACACTCGG
8525 8530	8535 8540	8545 8550	8555 8560	8565 8570	8575 8580
* *	* *	* *	* *	* *	* *
CAAGTGTGTA	GAAGAGTTAC	CTGAGTGCAA	TTTTGATGGC	TCTAGTACCT	TTCAGTCTGA
GTTACACAT	CTTCTCAATG	GACTCACCTT	AAAACCTACG	AGATCATGGA	AAGTCAGACT
8585 8690	8595 9600	8605 8610	8615 8620	8625 8630	8635 8640
* *	* *	* *	* *	* *	* *
GGGCTCCAAC	AGTGACATGT	ATCTCAGCCC	TGTTGCCATG	TTTCGGGACC	CCTTCCGCAG
CCCGAGGTTG	TCACTGTACA	TAGAGTCGGG	ACAACGGTAC	AAAGCCCTGG	GGAAGGCGTC

FIG. 29L

8645 8650	8655 8660	8665 8670	8675 8680	8685 8690	8695 8700
* *	* *	* *	* *	* *	* *
AGATCCCAAC	AAGCTGGTGT	TCTGTGAAGT	TTTCAAGTAC	AACCGGAAGC	CTGCAGAGAC
TCTAGGGTTG	TTCGACCACA	AGACACTTCA	AAAGTTCATG	TTGGCCTTCG	GACGTCTCTG
8705 8710	8715 8720	8725 8730	8735 8740	8745 8750	8755 8760
* *	* *	* *	* *	* *	* *
CAATTTAAGG	CACTCGTGTA	AACGGATAAT	GGACATGGTG	AGCAACCAGC	ACCCCTGGTT
GTAAATTC	GTGAGCACAT	TTGCCTATTA	CCTGTACCAC	TCGTTGGTCG	TGGGGACCAA
8765 8770	8775 8780	8785 8790	8795 8800	8805 8810	8815 8820
* *	* *	* *	* *	* *	* *
TGGAATGGAA	CAGGAGTATA	CTCTGATGGG	AACAGATGGG	CACCCCTTTT	GTTGGCCTTC
ACCTTACCTT	GTCCTCATAT	GAGACTACCC	TTGTCTACCC	GTGGGAAAAC	CAACCGGAAG
8825 8830	8835 8840	8845 8850	8855 8860	8865 8870	8875 8880
* *	* *	* *	* *	* *	* *
CAATGGCTTT	CCTGGGCCCC	AAGGTCCGTA	TTACTGTGGT	GTGGGCGCAG	ACAAAGCCTA
GTTACCGAAA	GGACCCGGGG	TTCCAGGCAT	AATGACACCA	CACCCGCGTC	TGTTTCGGAT
8885 8890	8895 8900	8905 8910	8915 8920	8925 8930	8935 8940
* *	* *	* *	* *	* *	* *
TGGCAGGGAT	ATCGTGGAGG	CTCACTACCG	CGCCTGCTTG	TATGCTGGGG	TCAAGATTAC
ACCGTCCCTA	TAGCACCTCC	GAGTGATGGC	GCGGACGAAC	ATACGACCCC	AGTTCTAATG
8945 8950	8955 8960	8965 8970	8975 8980	8985 8990	8995 9000
* *	* *	* *	* *	* *	* *
AGGAACAAAT	GCTGAGGTCA	TGCCTGCCCC	GTGGGAACTC	CAAATAGGAC	CCTGTGAAGG
TCCTTGTTTA	CGACTCCAGT	ACGGACGGGT	CACCCCTTGAG	GTTTATCCTG	GGACACTTCC
9005 9010	9015 9020	9025 9030	9035 9040	9045 9050	9055 9060
* *	* *	* *	* *	* *	* *
AATCCGCATG	GGAGATCATC	TCTGGGTGGC	CCGTTTCATC	TTNCATCGAG	TATGTGAAGA
TTAGGCGTAC	CCTCTAGTAG	AGACCCACCG	GGCAAACCTAG	AANGTAGCTC	ATACACTTCT
9065 9070	9075 9080	9085 9090	9095 9100	9105 9110	9115 9120
* *	* *	* *	* *	* *	* *
CTTTGGGGTA	ATAGCAACCT	TTGACCCCAA	GCCCATTCTT	GGGAACTGGA	ATGGTGCAGG
GAAACCCCAT	TATCGTTGGA	AACTGGGGTT	CGGGTAAGGA	CCCTTGACCT	TACCACGTCC
9125 9130	9135 9140	9145 9150	9155 9160	9165 9170	9175 9180
* *	* *	* *	* *	* *	* *
CTGCCATACC	AACTTTAGCA	CCAAGGCCAT	GCGGGAGGAG	AATGGTCTGA	AGCACATCGA
GACGGTATGG	TTGAAATCGT	GTTTCCGGTA	CGCCCTCCTC	TTACCAGACT	TCGTGTAGCT
9185 9190	9195 9200	9205 9210	9215 9220	9225 9230	9235 9240
* *	* *	* *	* *	* *	* *
GGAGGCCATC	GAGAAACTAA	GCAAGCGGCA	CCGGTACCAC	ATTGAGGCCT	ACGATCCCAA
CCTCCGGTAG	CTCTTTGATT	CGTTCGCCGT	GGCCATGGTG	TAAGCTCGGA	TGCTAGGGTT
9245 9250	9255 9260	9265 9270	9275 9280	9285 9290	9295 9300
* *	* *	* *	* *	* *	* *
GGGGGGCCTG	GACAATGCCC	GTGGTCTGAC	TGGGTTCCAC	GAAACGTCCA	ACATCAACGA
CCCCCGGAC	CTGTTACGGG	CACCAGACTG	ACCCAAGGTG	CTTTGCAGGT	TGTAGTTGCT
9305 9310	9315 9320	9325 9330	9335 9340	9345 9350	9355 9360
* *	* *	* *	* *	* *	* *
CTTTTCTGCT	GGTGTCGCCA	ATCGCAGTGC	CAGCATCCGC	ATTCCCCGGA	CTGTCGGCCA
GAAAAGACGA	CCACAGCGGT	TAGCGTCACG	GTCGTAGGCG	TAAGGGGCCT	GACAGCCGGT

FIG. 29M

9365 9370	9375 9380	9385 9390	9395 9400	9405 9410	9415 9420
* *	* *	* *	* *	* *	* *
GGAGAAGAAA	GGTTACTTTG	AAGACCGCGG	CCCCTCTGCC	AATTGTGACC	CCTTTGCAGT
CCTCTTCTTT	CCAATGAAAC	TTCTGGCGCC	GGGAGACGG	TTAACACTGG	GGAAACGTCA
9425 9430	9435 9440	9445 9450	9455 9460	9465 9470	9475 9480
* *	* *	* *	* *	* *	* *
GACAGAAGCC	ATCGTCCGCA	CATGCCTTCT	CAATGAGACT	GGCCACGAGC	CCTTCCAATA
CTGTCTTCGG	TAGCAGGCGT	GTACGGAAGA	GTTACTCTGA	CCGGTGCTCG	GGAAGGTTAT
9485 9490	9495 9500	9505 9510	9515 9520	9525 9530	9535 9540
* *	* *	* *	* *	* *	* *
CAAAAACTAA	TTAGACTTTG	AGTGATCTTG	AGCCTTTCCT	AGTTCATCCC	ACCCCGCCCC
GTTTTTGATT	AATCTGAAAC	TCACTAGAAC	TCGGAAAGGA	TCAAGTAGGG	TGGGGCGGGG
9545 9550	9555 9560	9565 9570	9575 9580	9585 9590	9595 9600
* *	* *	* *	* *	* *	* *
AGAGAGATCT	TTGTGAAGGA	ACCTTACTTC	TGTGGTGTGA	CATAATTGGA	CAAACTACCT
TCTCTCTAGA	AACACTTCCT	TGGAATGAAG	ACACCACACT	GTATTAACCT	GTTTGATGGA
9605 9610	9615 9620	9625 9630	9635 9640	9645 9650	9655 9660
* *	* *	* *	* *	* *	* *
ACAGAGATTT	AAAGCTCTAA	GGTAAATATA	AAATTTTAA	GTGTATAATG	TGTTAAACTA
TGTCTCTAAA	TTTCGAGATT	CCATTTATAT	TTTAAAAATT	CACATATTAC	ACAATTTGAT
9665 9670	9675 9680	9685 9690	9695 9700	9705 9710	9715 9720
* *	* *	* *	* *	* *	* *
CTGATTCTAA	TTGTTTGTGT	ATTTTAGATT	CCAACCTATG	GAAGTATGTA	ATGGGAGCAG
GACTAAGATT	AACAAACACA	TAAAATCTAA	GGTTGGATAC	CTTGACTACT	TACCCTCGTC
9725 9730	9735 9740	9745 9750	9755 9760	9765 9770	9775 9780
* *	* *	* *	* *	* *	* *
TGGTGGAATG	CCTTTAATGA	GGAAAACCTG	TTTTGCTCAG	AAGAAATGCC	ATCTAGTGAT
ACCACCTTAC	GGAAATTACT	CCTTTTGGAC	AAAACGAGTC	TTCTTTACGG	TAGATCACTA
9785 9790	9795 9800	9805 9810	9815 9820	9825 9830	9835 9840
* *	* *	* *	* *	* *	* *
GATGAGGCTA	CTGCTGACTC	TCAACATTCT	ACTCCTCCAA	AAAAGAAGAG	AAAGGTAGAA
CTACTCCGAT	GACGACTGAG	AGTTGTAAGA	TGAGGAGGTT	TTTTCTTCTC	TTTCCATCTT
9845 9850	9855 9860	9865 9870	9875 9880	9885 9890	9895 9900
* *	* *	* *	* *	* *	* *
GACCCCAAGG	ACTTTCCTTC	AGAATTGCTA	AGTTTTTTTGA	GTCATGCTGT	GTTTAGTAAT
CTGGGGTTCC	TGAAAGGAAG	TCTTAACGAT	TCAAAAAACT	CAGTACGACA	CAAATCATT
9905 9910	9915 9920	9925 9930	9935 9940	9945 9950	9955 9960
* *	* *	* *	* *	* *	* *
AGAACTCTTG	CTTGCTTTGC	TATTTACACC	ACAAAGGAAA	AAGCTGCACT	GCTATACAAG
TCTTGAGAAC	GAACGAAACG	ATAAATGTGG	TGTTTCCTTT	TTGACGTGA	CGATATGTTC
9965 9970	9975 9980	9985 9990	999610000	1000510010	1001510020
* *	* *	* *	* *	* *	* *
AAAATTATGG	AAAAATATTC	TGTAACCTTT	ATAAGTAGGC	ATAACAGTTA	TAATCATAAC
TTTTAATACC	TTTTTATAAG	ACATTGGAAA	TATTCATCCG	TATTGTCAAT	ATTAGTATTG
1002510030	1003510040	1004510050	1005510060	1006510070	1007510080
* *	* *	* *	* *	* *	* *
ATACTGTTTT	TTCTTACTCC	ACACAGGCAT	AGAGTGTCTG	CTATTAAATA	CTATGCTCAA
TATGACAAAA	AAGAATGAGG	TGTGTCCGTA	TCTCACAGAC	GATAATTATT	GATACGAGTT

FIG. 29N

1008510090	1009510100	1010510110	1011510120	1012510130	1013510140
*	*	*	*	*	*
AAATTGTGTA	CCTTTAGCTT	TTTAATTTGT	AAAGGGGTTA	ATAAGGAATA	TTTGATGTAT
TTTAACACAT	GGAAATCGAA	AAATTAAACA	TTTCCCAAT	TATTCCTTAT	AAACTACATA
1014510150	1015510160	1016510170	1017510180	1018510190	1019510200
*	*	*	*	*	*
AGTGCCTTGA	CTAGAGATCA	TAATCAGCCA	TACCACATTT	GTAGAGGTTT	TACTTGCTTT
TCACGGAAC	GATCTCTAGT	ATTAGTCGGT	ATGGTGTA	CATCTCCAAA	ATGAACGAAA
1020510210	1021510220	1022510230	1023510240	1024510250	1025510260
*	*	*	*	*	*
AAAAAACCTC	CCACACCTCC	CCCTGAACCT	GAAACATAAA	ATGAATGCAA	TTGTTGTTGT
TTTTTTGGAG	GGTGTGGAGG	GGGACTTGGA	CTTTGTATTT	TACTTACGTT	AACAACAACA
1026510270	1027510280	1028510290	1029510300	1030510310	1031510320
*	*	*	*	*	*
TAACCTGTTT	ATTGCAGCTT	ATAATGGTTA	CAAATAAAGC	AATAGCATCA	CAAATTTTAC
ATTGAACAAA	TAACGTCGAA	TATTACCAAT	GTTTATTTTCG	TTATCGTAGT	GTTTAAAGTG
1032510330	1033510340	1034510350	1035510360	1036510370	1037510380
*	*	*	*	*	*
AAATAAAGCA	TTTTTTTTCAC	TGCATTCTAG	TTGTGGTTTG	TCCAAACTCA	TCAATGTATC
TTTATTTTCG	AAAAAAAGTG	ACGTAAGATC	AACACCAAAC	AGGTTTGAGT	AGTTACATAG
1038510390	1039510400	1040510410	1041510420	1042510430	1043510440
*	*	*	*	*	*
TTATCATGTC	TGGATCTCTA	GCTTCGTGTC	AAGGACGGTG	ACTGCAGTGA	ATAATAAAAT
AATAGTACAG	ACCTAGAGAT	CGAAGCACAG	TTCTGCCAC	TGACGTCAC	TATTATTTTA
1044510450	1045510460	1046510470	1047510480	1048510490	1049510500
*	*	*	*	*	*
GTGTGTTTGT	CCGAAATACG	CGTTTTGAGA	TTTCTGTGCG	CGACTAAATT	CATGTCGCGC
CACACAAACA	GGCTTTATGC	GCAAACTCT	AAAGACAGCG	GCTGATTAA	GTACAGCGCG
1050510510	1051510520	1052510530	1053510540	1054510550	1055510560
*	*	*	*	*	*
GATAGTGGTG	TTTATCGCCG	ATAGAGATGG	CGATATTGGA	AAAATCGATA	TTTGAAAATA
CTATCACCAC	AAATAGCGGC	TATCTCTACC	GCTATAACCT	TTTTAGCTAT	AACTTTTAT
1056510570	1057510580	1058510590	1059510600	1060510610	1061510620
*	*	*	*	*	*
TGGCATATTG	AAAATGTGCG	CGATGTGAGT	TTCTGTGTAA	CTGATATCGC	CATTTTTC
ACCGTATAAC	TTTACAGCG	GCTACACTCA	AAGACACATT	GAATATAGCG	GTAAAAAGGT
1062510630	1063510640	1064510650	1065510660	1066510670	1067510680
*	*	*	*	*	*
AAAGTGATTT	TTGGGCATAC	GCGATATCTG	GCGATAGCGC	TTATATCGTT	TACGGGGGAT
TTTCACTAAA	AACCCGTATG	CGCTATAGAC	CGCTATCGCG	AATATAGCAA	ATGCCCCCTA
1068510690	1069510700	1070510710	1071510720	1072510730	1073510740
*	*	*	*	*	*
GGCGATAGAC	GACTTTGGTG	ACTTGGGCGA	TTCTGTGTGT	CGCAAATATC	GCAGTTTTCG
CCGCTATCTG	CTGAAACCAC	TGAACCCGCT	AAGACACACA	GCGTTTATAG	CGTCAAAGCT
1074510750	1075510760	1076510770	1077510780	1078510790	1079510800
*	*	*	*	*	*
TATAGGTGAC	AGACGATATG	AGGCTATATC	GCCGATAGAG	GCGACATCAA	GCTGGCACAT
ATATCCACTG	TCTGCTATAC	TCCGATATAG	CGGCTATCTC	CGCTGTAGTT	CGACCGTGTA

FIG. 290

1080510810	1081510820	1082510830	1083510840	1084510850	1085510860
* *	* *	* *	* *	* *	* *
GGCCAATGCA	TATCGATCTA	TACATTGAAT	CAATATTGGC	CATTAGCCAT	ATTATTTCATT
CCGGTTACGT	ATAGCTAGAT	ATGTAACCTA	GTTATAACCG	GTAATCGGTA	TAATAAGTAA
1086510870	1087510880	1088510890	1089510900	1090510910	1091510920
* *	* *	* *	* *	* *	* *
GGTTATATAG	CATAAATCAA	TATTGGCTAT	TGGCCATTGC	ATACGTTGTA	TCCATATCAT
CCAATATATC	GTATTTAGTT	ATAACCGATA	ACCGGTAACG	TATGCAACAT	AGGTATAGTA
1092510930	1093510940	1094510950	1095510960	1096510970	1097510980
* *	* *	* *	* *	* *	* *
AATATGTACA	TTTATATTGG	CTCATGTCCA	ACATTACCGC	CATGTTGACA	TTGATTATTG
TTATACATGT	AAATATAACC	GAGTACAGGT	TGTAATGGCG	GTACAACTGT	AACTAATAAC
1098510990	1099511000	1100511010	1101511020	1102511030	1103511040
* *	* *	* *	* *	* *	* *
ACTAGTTATT	AATAGTAATC	AATTACGGGG	TCATTAGTTC	ATAGCCCATA	TATGGAGTTC
TGATCAATAA	TTATCATTAG	TTAATGCCCC	AGTAATCAAG	TATCGGGTAT	ATACCTCAAG
1104511050	1105511060	1106511070	1107511080	1108511090	1109511100
* *	* *	* *	* *	* *	* *
CGCGTTACAT	AACTTACGGT	AAATGGCCCC	CCTGGCTGAC	CGCCCAACGA	CCCCCGCCCA
GCGCAATGTA	TTGAATGCCA	TTTACCGGGC	GGACCGACTG	GCGGGTTGCT	GGGGGCGGGT
1110511110	1111511120	1112511130	1113511140	1114511150	1115511160
* *	* *	* *	* *	* *	* *
TTGACGTCAA	TAATGACGTA	TGTTCCCATTA	GTAACGCCAA	TAGGGACTTT	CCATTGACGT
AACTGCAGTT	ATTACTGCAT	ACAAGGGTAT	CATTGCGGTT	ATCCCTGAAA	GGTAACTGCA
1116511170	1117511180	1118511190	1119511220	1120511210	1121511220
* *	* *	* *	* *	* *	* *
CAATGGGTGG	AGTATTTACG	GTAAACTGCC	CACTTGGCAG	TACATCAAGT	GTATCATATG
GTTACCCACC	TCATAAATGC	CATTTGACGG	GTGAACCGTC	ATGTAGTTCA	CATAGTATAC
1122511230	1123511240	1124511250	1125511260	1126511270	1127511280
* *	* *	* *	* *	* *	* *
CCAAGTACGC	CCCCTATTGA	CGTCAATGAC	GGTAAATGGC	CCGCCTGGCA	TTATGCCCAG
GGTTCATGCG	GGGGATAACT	GCAGTTACTG	CCATTTACCG	GGCGGACCGT	AATACGGGTC
1128511290	1129511300	1130511310	1131511320	1132511330	1133511340
* *	* *	* *	* *	* *	* *
TACATGACCT	TATGGGACTT	TCCTACTTGG	CAGTACATCT	ACGTATTAGT	CATCGCTATT
ATGTACTGGA	ATACCCTGAA	AGGATGAACC	GTCATGTAGA	TGCATAATCA	GTAGCGATAA
1134511350	1135511360	1136511370	1137511380	1138511390	1139511400
* *	* *	* *	* *	* *	* *
ACCATGGTGA	TGCGGTTTTG	GCAGTACATC	AATGGGCGTG	GATAGCGGTT	TGACTCACGG
TGGTACCACT	ACGCCAAAAC	CGTCATGTAG	TTACCCGCAC	CTATCGCCAA	ACTGAGTGCC
1140511410	1141511420	1142511430	1143511440	1144511450	1145511460
* *	* *	* *	* *	* *	* *
GGATTTCCAA	GTCTCCACCC	CATTGACGTC	AATGGGAGTT	TGTTTTGGCA	CCAAAATCAA
CCTAAAGGTT	CAGAGGTGGG	GTAACCTGAG	TTACCCCTCAA	ACAAAACCGT	GTTTTTAGTT
1146511470	1147511480	1148511490	1149511500	1150511510	1151511520
* *	* *	* *	* *	* *	* *
CGGGACTTTC	CAAAAATGTCG	TAACAACCTCC	GCCCCATTGA	CGCAAATGGG	CGGTAGGCGT
GCCCTGAAAG	GTTTTACAGC	ATTGTTGAGG	CGGGGTAACT	GCGTTTACCC	GCCATCCGCA

FIG. 29P

1152511530	1153511540	1154511550	1155511560	1156511570	1157511580
* *	* *	* *	* *	* *	* *
GTACGGTGGG	AGGTCTATAT	AAGCAGAGCT	CGTTTATGTA	ACCGTCAGAT	CGCCTGGAGA
CATGCCACCC	TCCAGATATA	TTCGTCTCGA	GCAAATCACT	TGGCAGTCTA	GCGGACCTCT
1158511590	1159511600	1160511610	1161511620	1162511630	1163511640
* *	* *	* *	* *	* *	* *
CGCCATCCAC	GCTGTTTTGA	CCTCCATAGA	AGACACCGGG	ACCGATCCAG	CCTCCGCGGC
GCGGTAGGTG	CGACAAAAC	GGAGGTATCT	TCTGTGGCCC	TGGCTAGGTC	GGAGGCGCCG
1164511650	1165511660	1166511670	1167511680	1168511690	1169511700
* *	* *	* *	* *	* *	* *
CGGGAACGGT	GCATTGGAAC	GCGGATTCCC	CGTGCCAAGA	GTGACGTAAG	TACCGCCTAT
GCCCTTGCCA	CGTAACCTTG	CGCCTAAGGG	GCACGGTTCT	CACTGCATTC	ATGGCGGATA
1170511710	1171511720	1172511730	1173511740	1174511750	1175511760
* *	* *	* *	* *	* *	* *
AGAGTCTATA	GGCCACCCCC	CTTGGCTTCT	TATGCATGCT	ATACTGTTTT	TGGCTTGGGG
TCTCAGATAT	CCGGGTGGGG	GAACCGAAGA	ATACGTACGA	TATGACAAAA	ACCGAACCCC
1176511770	1177511780	1178511790	1179511800	1180511810	1181511820
* *	* *	* *	* *	* *	* *
TCTATACACC	CCCGCTTCCT	CATGTTATAG	GTGATGGTAT	AGCTTAGCCT	ATAGGTGTGG
AGATATGTGG	GGGCGAAGGA	GTACAATATC	CACTACCATA	TCGAATCGGA	TATCCACACC
1182511830	1183511840	1184511850	1185511860	1186511870	1187511880
* *	* *	* *	* *	* *	* *
GTTATTGACC	ATTATTGACC	ACTCCCCTAT	TGGTGACGAT	ACTTTCATT	ACTAATCCAT
CAATAACTGG	TAATAACTGG	TGAGGGGATA	ACCACTGCTA	TGAAAGGTAA	TGATTAGGTA
1188511890	1189511900	1190511910	1191511920	1192511930	1193511940
* *	* *	* *	* *	* *	* *
AACATGGCTC	TTTGCCACAA	CTCTCTTTAT	TGGCTATATG	CCAATACACT	GTCCTTCAGA
TTGTACCGAG	AAACGGTGTT	GAGAGAAATA	ACCGATATAC	GGTTATGTGA	CAGGAAGTCT
1194511950	1195511960	1196511970	1197511980	1198511990	1199512000
* *	* *	* *	* *	* *	* *
GA CTGACACG	GACTCTGTAT	TTTTACAGGA	TGGGGTCTCA	TTTATTATTT	ACAAATTCAC
CTGACTGTGC	CTGAGACATA	AAAATGTCCT	ACCCAGAGT	AAATAATAAA	TGTTTAAAGTG
1200512010	1201512020	1202512030	1203512040	1204512050	1205512060
* *	* *	* *	* *	* *	* *
ATATACAACA	CCACCGTCCC	CAGTGCCCGC	AGTTTTTATT	AAACATAACG	TGGGATCTCC
TATATGTTGT	GGTGGCAGGG	GTCACGGGCG	TCAAAAATAA	TTTGTATTGC	ACCCTAGAGG
1206512070	1207512080	1208512090	1209512100	1210512110	1211512120
* *	* *	* *	* *	* *	* *
ACGCGAATCT	CGGGTACGTG	TTCCGGACAT	GGGCTCTTCT	CCGGTAGCGG	CGGAGCTTCT
TGCGCTTAGA	GCCCATGCAC	AAGGCCTGTA	CCCAGAGAAG	GGCCATCGCC	GCCTCGAAGA
1212512130	1213512140	1214512150	1215512160	1216512170	1217512180
* *	* *	* *	* *	* *	* *
ACATCCGAGC	CCTGCTCCCA	TGCCTCCAGC	GACTCATGGT	CGCTCGGCAG	CTCCTTGCTC
TGTAGGCTCG	GGACGAGGGT	ACGGAGGTCG	CTGAGTACCA	GCGAGCCGTC	GAGGAACGAG
1218512190	1219512200	1220512210	1221512220	1222512230	1223512240
* *	* *	* *	* *	* *	* *
CTAACAGTGG	AGGCCAGACT	TAGGCACAGC	ACGATGCCCC	CCACCACCAG	TGTGCCGCAC
GATTGTCACC	TCCGGTCTGA	ATCCGTGTCG	TGCTACGGGT	GGTGGTGGTC	ACACGGCGTG

FIG. 29Q

1224512250	1225512260	1226512270	1227512280	1228512290	1229512300
*	*	*	*	*	*
AAGGCCGTGG	CGGTAGGGTA	TGTGTCTGAA	AATGAGCTCG	GGGAGCGGGC	TTGCACCGCT
TTCCGGCACC	GCCATCCCAT	ACACAGACTT	TTACTCGAGC	CCCTCGCCCG	AACGTGGCGA
1230512310	1231512320	1232512330	1233512340	1234512350	1235512360
*	*	*	*	*	*
GACGCATTTG	GAAGACTTAA	GGCAGCGGCA	GAAGAAGATG	CAGGCAGCTG	AGTTGTTGTG
CTGCGTAAAC	CTTCTGAATT	CCGTCGCCGT	CTTCTTCTAC	GTCCGTCGAC	TCAACAACAC
1236512370	1237512380	1238512390	1239512400	1240412410	1241512420
*	*	*	*	*	*
TTCTGATAAG	AGTCAGAGGT	AACTCCCGTT	GCGGTGCTGT	TAACGGTGGA	GGGCAGTGTA
AAGACTATTC	TCAGTCTCCA	TTGAGGGCAA	CGCCACGACA	ATTGCCACCT	CCCGTCACAT
1242512430	1243512440	1244512450	1245512460	1246512470	1247512480
*	*	*	*	*	*
GTCTGAGCAG	TACTCGTTGC	TGCCGCGCGC	GCCACCAGAC	ATAATAGCTG	ACAGACTAAC
CAGACTCGTC	ATGAGCAACG	ACGGCGCGCG	CGGTGGTCTG	TATTATCGAC	TGTCTGATTG
1248512490	1249512500	1250512510	1251512520	1252512530	1253512540
*	*	*	*	*	*
AGACTGTTCC	TTTCCATGGG	TCTTTTCTGC	AGTCACCGTC	CTTGACACGA	AGCTTACCAT
TCTGACAAGG	AAAGGTACCC	AGAAAAGACG	TCAGTGGCAG	GAAGTGTGCT	TCGAATGGTA
1254512550	1255512560	1256512570	1257512580	1258512590	1259512600
*	*	*	*	*	*
GGGTGTGCCC	ACTCAGGTCC	TGGGGTTGCT	GCTGCTGTGG	CTTACAGATG	CCAGATGTGA
CCCACACGGG	TGAGTCCAGG	ACCCCAACGA	CGACGACACC	GAATGTCTAC	GGTCTACACT
1260512610	1261512620	1262512630	1263512640	1264512650	1265512660
*	*	*	*	*	*
GATCGTTCTC	ACGCAGTCTC	CAGGCACCCT	GTCTCTGTCT	CCAGGGGAAA	GAGCCACCTT
CTAGCAAGAG	TGCGTCAGAG	GTCCGTGGGA	CAGAGACAGA	GGTCCCCTTT	CTCGGTGGAA
1266512670	1267512680	1268512690	1269512700	1270512710	1271512720
*	*	*	*	*	*
CTCCTGTAGG	TCCAGTCACA	GCATTTCGAG	CCGCCGCGTA	GCCTGGTACC	AGCACAAACC
GAGGACATCC	AGGTCAGTGT	CGTAAGCGTC	GGCGGCGCAT	CGGACCATGG	TCGTGTTTGG
1272512730	1273512740	1274512750	1275512760	1276512770	1277512780
*	*	*	*	*	*
TGGCCAGGCT	CCAAGGCTGG	TCATACATGG	TGTTTCCAAT	AGGGCCTCTG	GCATCTCAGA
ACCGGTCCGA	GGTTCCGACC	AGTATGTACC	ACAAAGGTTA	TCCCGGAGAC	CCTAGAGTCT
1278512790	1279512800	1280512810	1281512820	1282512830	1283512840
*	*	*	*	*	*
CAGGTTTCAGC	GGCAGTGGGT	CTGGGACAGA	CTTCACTCTC	ACCATCACCA	GAGTGGAGCC
GTCCAAGTCG	CCGTCAACCA	GACCTGTCT	GAAGTGAGAG	TGGTAGTGGT	CTCACCTCGG
1284512850	1285512860	1286512870	1287512880	1288512890	1289512900
*	*	*	*	*	*
TGAAGACTTT	GCACTGTAAT	ACTGTCAGGT	CTATGGTGCC	TCCTCGTACA	CTTTTGGCCA
ACTTCTGAAA	CGTGACATGA	TGACAGTCCA	GATACCACGG	AGGAGCATGT	GAAAACCGGT
1290512910	1291512920	1292512930	1293512940	1294512950	1295512960
*	*	*	*	*	*
GGGGACCAAA	CTGGAGAGGA	AACGAACTGT	GCCTGCACCA	TCTGTCTTCA	TCTTCCCGCC
CCCCTGGTTT	GACCTCTCCT	TTGCTTGACA	CGGACGTGGT	AGACAGAAAGT	AGAAGGGCGG

FIG. 29R

1296512970	1297512980	1298512990	1299513000	1300513010	1301513020
*	*	*	*	*	*
ATCTGATGAG	CAGTTGAAAT	CTGGGACTGC	CTCTGTTGTG	TGCCTGCTGA	ATAACTTCTA
TAGACTACTC	GTCAACTTTA	GACCCTGACG	GAGACAACAC	ACGGACGACT	TATTGAAGAT
1302513030	1303513040	1304513050	1305513060	1306513070	1307513080
*	*	*	*	*	*
TCCCAGAGAG	GCCAAAGTAC	AGTGGAAGGT	GGATAACGCC	CTCCAATCGG	GTAAC TCCCA
AGGGTCTCTC	CGGTTTCATG	TCACCTTCCA	CCTATTGCGG	GAGGTTAGCC	CATTGAGGGT
1308513090	1309513100	1310513110	1311513120	1312513130	1313513140
*	*	*	*	*	*
GGAGAGTGTC	ACAGAGCAGG	ACAGCAAGGA	CAGCACCTAC	AGCCTCAGCA	GCACCCTGAC
CCTCTCACAG	TGTCTCGTCC	TGTCGTTTCT	GTCGTGGATG	TCGGAGTCGT	CGTGGGACTG
1314513150	1315513160	1316513170	1317513180	1318513190	1319513200
*	*	*	*	*	*
GCTGAGCAAA	GCAGACTACG	AGAAACACAA	AGTCTACGCC	TGCGAAGTCA	CCCATCAGGG
CGACTCGTTT	CGTCTGATGC	TCTTTGTGTT	TCAGATGCGG	ACGCTTCAGT	GGGTAGTCCC
1320513210	1321513220	1322513230	1323513240	1324513250	13255
*	*	*	*	*	
CCTGAGATCG	CCCGTCACAA	AGAGCTTCAA	CAGGGGAGAG	TGTTAATTCT	AGAGAA
GGACTCTAGC	GGGCAGTGTT	TCTCGAAGTT	GTCCCCTCTC	ACAATTAAGA	TCTCTT

FIG. 29S